

Result No.	Score	Query Match Length	DB ID	Description
1	1116	100	0 212 17 AAR98224	Hypoxanthine guanine transferase
2	1069	95	8 225 21 AAB94995	Human protein sequ
3	1065	95	4 225 22 AABP41467	Human ovarian anti
4	1065	95	4 230 23 AABP41467	Mouse Hprt. Mus m
5	772	69	2 218 18 AAW37339	P. falciparum Hgpr
6	445.5	39	9 231 22 AAB85165	Lactococcus lactis
7	265.5	23	8 180 23 ABB54862	Lactococcus lactis
8	23.4	23	8 183 23 ABB53319	'Streptococcus poly
9	23.1	23	8 180 23 ABBP21993	'Streptococcus poly

red. $No.$ is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	1116	100.0	212	17 AAR98224	Hypoxanthine Guanine phosphoribosyltransferase
2	1069	95.8	225	21 AAY79112	Human protein sequ
3	1065	95.4	225	22 AAB94995	Human ovarian anti
4	1065	95.4	230	23 ABP41467	Mouse Hprt. Mus m
5	772	69.2	218	18 AAW37739	P. falciparum Hprt
6	445.5	39.9	231	22 AAB85165	Lactococcus lactis
7	265.5	23.8	180	23 ABP51862	Lactococcus lactis
8	261	23.4	183	23 ABP53219	'Streptococcus poly
9	257.5	23.1	180	23 ABP21993	DR N-PSDB; AAT30127.

PT DNA encoding human hypoxanthine guanine phosphoribosyl transferase
 PT 2 - provides a polypeptide capable of therapeutic end use in purine
 PT synthesis disorders
 XX
 PS Claim 14: Page 33-34; 50PP; English.

XX Human hypoxanthine (guanine) phosphoribosyl transferase 2 (HPRT-2) (AAR8224) is utilised by mammalian cells for the salvage of purines, preventing the formation of uric acid. Its amino acid sequence was deduced from a cDNA clone (AA730127) isolated from a foetal lung library. Recombinant HPRT-2 can be expressed in prokaryotic or eukaryotic (e.g. COS, SF9) host cells. It can be used to prevent or treat Lesch-Nyhan syndrome, kidney stones, renal failure, uricaciduria, precocious gout, anaemia and nephrolithiasis. It is also used to screen for HPRT-2 antagonists and to raise antibodies.

XX Sequence 212 AA;

SQ Query Match 100.0%; Score 1116; DB 17; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATRSPGVVINDDWPGYDNLNFTYPQHYGGDLEYVLIPIHGLIVDIERLAKIDMDIGS 60
 1 MATRSPGVVINDDWPGYDNLNFTYPQHYGGDLEYVLIPIHGLIVDIERLAKIDMDIGS 60
 Qy 61 DIMVLCVLRGGKFCADLVEHKNIKNSDRFVSMKVDFIRLKSYNDQSGEMQIIGGG 120
 61 DIMVLCVLRGGKFCADLVEHKNIKNSDRFVSMKVDFIRLKSYNDQSGEMQIIGGG 120
 Db 121 DLSTLACKNFTLIVEDVYGTGRTGMKALLSIEKYPNMIKVASLLVRTSRSDGFRDYAG 180
 121 DLSTLACKNFTLIVEDVYGTGRTGMKALLSIEKYPNMIKVASLLVRTSRSDGFRDYAG 180
 Qy 181 FEIPLHFVVGAYALDNEYFRDLNHCIVINEHG 212
 181 FEIPLHFVVGAYALDNEYFRDLNHCIVINEHG 212
 Db 181 FEIPLHFVVGAYALDNEYFRDLNHCIVINEHG 212

RESULT 2
 AAY79212
 ID AAY79212 standard; Protein: 225 AA.
 XX
 AC AAY79212;
 XX DT 19-JUN-2000 (first entry)
 XX Human transferase TRNSFS-4.

KW Transferase; TRNSFS-4; human; antitumour; cancer;
 KW Gastrointestinal disorder; developmental disorder;
 KW genetic disorder; neurological disorder; reproductive disorder;
 KW smooth muscle disorder; immunological disorder; inflammation;
 KW diagnosis; hypoxanthine (guanosine) phosphoribosyltransferase;
 KW therapy.

XX Homo sapiens.

XX Key
 PT Modified-site 176
 PT Modified-site 4
 PT Modified-site 117
 PT Modified-site 155
 PT Modified-site 96
 PT Modified-site 101
 PT Modified-site 111

/note= "potential O-phosphorylation"
 /note= "potential O-phosphorylation"

Location/Qualifiers
 14 GVVIMDDWPGYDNLNFTYPQHYGGDLEYVLIPIHGLIVDIERLAKIDMDIGS 66
 14 GVVIMDDWPGYDNLNFTYPQHYGGDLEYVLIPIHGLIVDIERLAKIDMDIGS 73
 67 VLKGKGFKFCADLVEHKNIKNSDRFVSMKVDFIRLKSYNDQSGEMQIIGGGDSTLA 126
 74 VLKGKGFKFCADLVEHKNIKNSDRFVSMKVDFIRLKSYNDQSGEMQIIGGGDSTLA 133
 127 GKNFLIVEDVYGTGRTGMKALLSIEKYPNMIKVASLLVRTSRSDGFRDYAGFPIPHL 186
 134 GRNVLYALDNEYFRDLNHCIVINEHG 212

FT FT Modified-site 146
 FT FT Modified-site 149
 FT FT Modified-site 175
 FT FT Modified-site 91
 FT FT Domain 35 - 225
 /note= "purine/pyrimidine phosphoribosyltransferase domain"
 XX WO200014251-A2.
 PN XX
 PD XX
 PD 16-MAR-2000.
 XX
 PF 09-SEP-1999;
 XX 99WO-US20089.
 PR 10-SEP-1998;
 PR 04-NOV-1998;
 PR 11-MAY-1999;
 XX
 PA (INCYT-) INCYTE PHARM INC.
 PA Tang YT, Corley NC, Guegler KJ, Baughn MR, Lal P, Yue H;
 PI Hillman JL, Azzmazi Y;
 DR WPI: 2000-256996/22.
 DR N-PSDB; AA294204.

XX Human transferase proteins useful for preventing, diagnosing and treating cancers and developmental, gastrointestinal, genetic, immunological, neurological, reproductive and smooth muscle disorders -

PS Claim 1; Page 82-83; 113bp; English.

XX The present sequence is that of human transferase TRNSFS-4, 1 of 15 claimed novel human transferase proteins of the invention (see CC 15 claimed novel human transferase proteins of the invention (see CC AAY79209-23). The sequence was deduced from a cDNA clone (see CC AAZ9204) isolated from a myxoma tissue library. It shows homology CC to hypoxanthine (guanine) phosphoribosyltransferase. TRNSFS-4 is CC expressed in nervous, cardiovascular, gastrointestinal, reproductive, haematopoietic and nervous tissues, especially those CC associated with cancer and inflammation. The new human transferase CC proteins and the polynucleotides encoding them can be used in the CC diagnosis, prevention and treatment of cancer, developmental CC disorders, gastrointestinal disorders, genetic disorders, CC immunological disorders, neurological disorders, reproductive CC disorders, and smooth muscle disorders. The polypeptides can also CC be used to raise antibodies, and to screen for agonists and CC antagonists of transferase activity.

XX Sequence 225 AA;

Query Match 95.8%; Score 1069; DB 21; Length 225;
 Best Local Similarity 98.5%; Pred. No. 3.4e-110;
 Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GVVIMDDWPGYDNLNFTYPQHYGGDLEYVLIPIHGLIVDIERLAKIDMDIGS 66
 Db 14 GVVIMDDWPGYDNLNFTYPQHYGGDLEYVLIPIHGLIVDIERLAKIDMDIGS 73
 Qy 67 VLKGKGFKFCADLVEHKNIKNSDRFVSMKVDFIRLKSYNDQSGEMQIIGGGDSTLA 126
 Db 74 VLKGKGFKFCADLVEHKNIKNSDRFVSMKVDFIRLKSYNDQSGEMQIIGGGDSTLA 133
 Qy 127 GKNFLIVEDVYGTGRTGMKALLSIEKYPNMIKVASLLVRTSRSDGFRDYAGFPIPHL 186
 Db 134 GRNVLYALDNEYFRDLNHCIVINEHG 212

Qy 187 FVVGYALDNEYFRDLNHCIVINEHG 212

Db	194	FVVGAYLDNEYFRDLNHTICVINEHG	219	Db	14	GVVIMDDWPGYDLNLFTYPHYYGDLEYVLIPHGIIVDRERLANDIMKDIGYSDDIMVLC	73
RESULT 3							
AAB94995		Human protein sequence	SEQ ID NO:16623	QY	67	VLKGGXKFCADLVEILKNIERNSDFVSMKVDFTIKSYNDQSMEMQI1GGGDISTLA	126
ID	AAB94995	standard; Protein;	225 AA.	Db	74	VLKGGXKFCADLVEILKNIERNSDFVSMKVDFTIKSYNDQSMEMQI1GGGDISTLA	133
XX				QY	127	GKFLIVEDVGTGTMKALLSNIKYKPNMKVASSLLVKTTSRSGFRPDYAGFPIPHL	186
AC	AAB94995	XX		Db	134	GKFLIVEDVGTGTMKALLSNIKYKPNMKVASSLLVKTTSRSGFRPDYAGFPIPHL	193
XX	26-JUN-2001	(first entry)		QY	187	FVVGAYLDNEYFRDLNHTICVINEHG	212
DT				Db	194	FVVGAYLDNEYFRDLNHTICVINEHG	219
DE							
XX							
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy; gene therapy; gene therapy.						
XX							
OS	Homo sapiens.						
XX							
PN	EP1074617-A2.						
XX							
PD	07-FEB-2001.						
XX							
PF	28-JUL-2000; 20000EP-0116126.						
XX							
PR	29-JUL-1999; 99JP-024B036.						
XX							
PR	27-AUG-1999; 99JP-0302253.						
XX							
PR	11-JAN-2000; 20000EP-0118776.						
XX							
PR	02-MAY-2000; 20000EP-0133767.						
XX							
PR	09-JUN-2000; 20000EP-0241899.						
XX							
PA	(HELI-1) HELIX RES INST.						
XX							
PI	Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, T.;						
PI	Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T.;						
XX							
DR	WPI; 2001-318749/34.						
XX							
PT	Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -						
PT							
PT	Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -						
PT							
PS	Claim 8; SEQ ID 16623; 2537pp + CD ROM; English.						
XX							
CC	The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set						
CC	comprises: (a) an oligo-dT primer and an oligonucleotide which comprises one of						
CC	the 5602 nucleotide sequences defined in the specification, where the						
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination						
CC	of an oligonucleotide comprising a sequence complementary to the						
CC	complementary strand of a polynucleotide which comprises a 5'-end						
CC	sequence and an oligonucleotide comprising a sequence complementary to a						
CC	polynucleotide which comprises a 3'-end sequence, where the						
CC	oligonucleotide comprises at least 15 nucleotides and the combination of						
CC	the 5'-end sequence/3'-end sequence is selected from those defined in						
CC	the specification. The primer sets can be used in antisense therapy and						
CC	gene therapy. The primers are useful for synthesising polynucleotides,						
CC	particularly full-length cDNAs. The primers are also useful for the						
CC	detection and/or diagnosis of the abnormality of the proteins encoded by						
CC	the full-length cDNAs. The primers allow obtaining the full-length						
CC	cDNAs easily without any specialised methods. AAH1633 to AAH1628 and						
CC	AAH1633 to AAH1642 represent human cDNA sequences; AAB92446 to						
CC	AAB92446 to AAH13632 represent human amino acid sequences; and AAH13632						
CC	represent oligonucleotides, all of which are used in the exemplification						
CC	of the present invention.						
SQ	Sequence 225 AA;						
XX							
XX	Query Match 95.4%; Score 1065; DB 22; Length 225;						
XX	Best Local Similarity 98.5%; Pred. No. 9.5e-110;						
XX	Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;						
QY	7 GVVIMDDWPGYDLNLFTYPHYYGDLEYVLIPHGIIVDRERLANDIMKDIGYSDDIMVLC	66					

XX DR WPI: 2001-39658/42.
 XX DR N-PSDB; AAF84137, AAF84138.
 XX PT Plasmodium falciparum hypoxanthine-guanine phosphoribosyl transferase
 XX PT (HGPRT) enzyme for development of anti-malarials -
 XX PS Claim 1; Columns 7-9; 9pp; English.
 XX
 The invention provides a Plasmodium falciparum hypoxanthine-guanine phosphoribosyl transferase (HGPRT) enzyme, a dimeric protein with a molecular weight of about 52,000 daltons. Inhibitors of HGPRT may be utilized as standard recombinant methodology. Inhibitors of HGPRT can use xanthine as a substrate while the human form cannot. Therefor inhibitors will selectively inhibit HGPRT suppressing the growth of the parasite while allowing host immune responses to combat the infection. The present sequence represents the plasmid HGPRT enzyme.
 XX
 Sequence 231 AA;
 Query Match 39.9%; Score 445.5; DB 22; Length 231;
 Best Local Similarity 42.7%; Pred. No. 5.9e-41; Indels 11; Gaps 3;
 Matches 93; Conservative 40; Mismatches 74;
 QY 5 SPGV-----VIMDWPGYDNLFTYPOHYGYDLEYVILPHGIVDRAERLAKIDMKD1 57
 Db 6 NPGAGENAEDFWVFKDDGYDLSMTPAHTKTYLTKVLYVNGVAKNRERLADIKKY 65
 QY 58 GYSDDIMVLCVKGKFKCADLVEHLKNISRNDSRFVSMKV--DFIRLKSYRNDSGM 114
 Db 66 NNEEFHILCLLKGSRSFFTALLKHSRHNYSAVETSKPLFGEHYVRSYCNQDSTGTL 125
 QY 115 QIIGGGDLSTLAGKNFLIVEDVGTGTRMALLSNTIEKYKPNMIVKASLVLKRTSRSDG 174
 Db 126 EIV-SEDSLCLKGKHYLIVEDDTGKTLVKFCYIKTKVIAICLPIKRTPLWNGF 184
 QY 175 RPDYAGEIPTPHFLVFGYSDYKLDNEYFVFLNHCIVINPHG 212
 Db 185 KADFVGFSIPDHFVVGYSLDYNEIFRDLHDCCLVNDEG 222
 RESULT 7 ABB54862 standard; Protein; 180 AA.
 ID ABB54862 standard; Protein; 180 AA.
 XX AC ABB54862;
 XX DT 16-MAY-2002 (first entry)
 XX DB Lactococcus lactis protein hpt-
 XX AC Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 XX OS Lactococcus lactis IL1403.
 XX PN FR2807446-A1.
 XX PR 12-OCT-2001.
 XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 XX PR 11-APR-2000; 20000FR-0004630.
 XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 XX PR 11-APR-2000; 20000FR-0004630.
 XX DR WPI: 2002-043418/06.
 XX
 New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
 XX
 Claim 6: SEQ ID No 21; 2504pp; French.
 XX
 The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
 Note: The sequence data for this patent is based on equivalent patent WO20017334 (published 18-Oct-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 180 AA;
 Query Match 23.8%; Score 265.5; DB 23; Length 180;
 Best Local Similarity 35.4%; Pred. No. 4.1e-21;
 Matches 64; Conservative 38; Mismatches 66; Indels 13; Gaps 4;
 QY 32 LEVYLIPHGLIVDRIERLAKIDMKD1GYSDDIMVLCVKGKFKCADLVEHLKNISRNDSR 91
 5 LKEVLFTRREQIAERVKEAENVSRDYEGRNPLVVGILKGSIMPTVDLILKELS---- 56
 QY 92 FVSMKVDFLRLKSY-RNDOSGMQIIGGDLSTLA-GKNNFLIVEDVVTGTRTMKALLSN 149
 Db 57 -1DAEVFDMDVTSYGGISSSGSEVRL--KDLSTVAHGRDLIVEDIITGTNTLLYKKL 113
 QY 150 IEKYPNMIKVASLVLKRTSRSDGFRPDYAGFEPHFLFVGVYALDNEYFVDLNHICVYN 209
 Db 114 LTGQSARHSVKTISLUDKPSGRKVNDIDAFVGFIDADVGFEPDAFIVGQDIAEPRYRQLPYIGFPN 173
 RESULT 8 ABB53319 standard; Protein; 183 AA.
 ID ABB53319 standard; Protein; 183 AA.
 XX AC ABB53319;
 XX DT 16-MAY-2002 (first entry)
 XX DE Lactococcus lactis protein hpt.
 XX KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 XX OS Lactococcus lactis IL1403.
 XX PN FR2807446-A1.
 XX PR 12-OCT-2001.
 XX PD 11-APR-2000; 20000FR-0004630.
 XX PR 11-APR-2000; 20000FR-0004630.
 XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 XX PR 11-APR-2000; 20000FR-0004630.
 XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 XX PR 11-APR-2000; 20000FR-0004630.
 XX DR WPI: 2002-043418/06.
 XX
 New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
 XX
 Claim 6: SEQ ID No 21; 2504pp; French.
 XX
 The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
 Note: The sequence data for this patent is based on equivalent patent WO20017334 (published 18-Oct-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.

CC Note: The sequence data for this patent is based on equivalent patent

CC WO20017734 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 183 AA;

Qy 32 LEVYLPHGIIYDRIERLAKD1MKD1GYS1D1M1LCVUKGGKFCADLVEHILKN1SNSDR 91

Db 10 TEKVLVSEEEITKESKELGEILTKEYEGKNPLVGLRLGSYFLAELIKHD----- 61

Qy 92 FVSMKDF1RKLKSRY NDQSMEMQ1TQIGGDLSLTLAGKFLIVEDVVTGRTMKALLSN 150

Db 62 -CHLEIDEMTSSYHGGTQSSEVKKL1LDVD-TAVGRD1LIVED.D1DTGTLKYLKELL 119

Qy 151 EKYKPNM1KVASLLVKRTSRSDGERPDYAGFBIPLFVVGYALDYNEYFRDLNHCIV 208

Db 120 EHRGAN-VKIV1L1DPEGR1VEIKPDYSGFTIPNEFVGFLDVBENYRNLPYVGVL 176

RESULT 9
 ABP27993 ID ABP27993 standard; Protein; 180 AA.

XX AC ABP27993;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 5162.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX KW group A streptococci; Streptococcus pyogenes; antibacterial;

XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

OS Streptococcus pyogenes.

PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026332.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C,

PI Tettelin H,

XX WPI; 2002-352536/38.

DR N-PSDB; ABN68624.

XX New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3680; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), Given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

SQ Sequence 180 AA;

Qy 31 DLEYVILPHGIIYDRIERLAKD1MKD1GYS1D1M1LCVUKGGKFCADLVEHILKN1SNSDR 90

Db 5 DIQKILYSENDIIRKTKLGEQLTK1QEQKNPLM1GVLKG5VPFMELMKHID----- 57

Qy 91 RFVSMRVD1FIRLKSRY NDQSMEMQ1LQIGGDLSLAGKNFLIVEDVVTGRTMKALLSN 149

Db 58 --THVEIDEMVYSSYHGGTSSSGEYK1LKD1VDTGRTLKV1RDM 114

Qy 150 TEKYKPNM1KVASLLVKRTSRSDGERPDYAGFBIPLFVVGYALDYNEYFRDLNHCIVN 209

Db 115 FKYRKANTIKIATLFDKPEGRVVVKIADYVCYNIPNEFIVFGFLDVAENYRNLPYVGVLK 174

Qy 210 E 210

Db 175 E 175

RESULT 10

AAG92711

ID AAG92711 standard; Protein; 194 AA.

AC AAG92711;

XX DT 26-SEP-2001 (first entry)

XX DE C glutamicum protein fragment SEQ ID NO: 6465.

XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

XX KW organic acid synthesis.

XX OS Corynebacterium glutamicum.

XX PN EP1108790-A2.

XX PR 16-DEC-1999; 99JP-0377484.

XX PR 07-APR-2000; 2000JP-0159462.

XX PR 03-AUG-2000; 2000JP-0280388.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX PI Tateishi N, Sano A, Ikeda M, Ozaki A;

XX DR WPI; 2001-376911/40.

XX DR N-PSDB; ABH67930.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT

This represents a *S. pneumoniae* putative ATPase involved in membrane functions. The invention provides DNA sequences (AAV65201 to AAV65304) from the Streptococcus pneumoniae genome and corresponding protein sequences (AAW8005 to AAW80728). The protein sequences are classified as hypothetical, cell wall biosynthetic, external target, or minimal gene set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragments of any one or more of these DNA sequences. The DNA chip can be used for evaluating gene expression in *S. pneumoniae* and for identifying virulence genes in *S. pneumoniae*. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat *S. pneumoniae* infection. The antibodies can also be used to detect *S. pneumoniae* cells.

Sequence 180 AA;

Query	31 DLEYVLIPHGIIVDRIBLAKIMKDGYSDIMVLCKLGGKFKCADLVEHARNTSNSD 90
Db	5 DIKKVLVSHDETEAAKLGQLTKDYAGKNTLVLGKGSIPPEMAELVKHI-----D 57
Qy	91 RFVSMKVYDFIRLKSYRNDQSMGEMQIIGGGDLSLTLAKRNFLIVEDVYGTGRTMKALLSNI 150
Db	58 THIEM- DFMVMTSSYRGTASSGVINIKQDVTQDIKEFVQTLKNDRMF 115
Qy	151 EKYKPNMVKAVSLLVKRTSRSDGFRPDYAGFELPHLFLVGVYALDNEYFDRDLNHCYINE 210
Db	116 KEREAAVSVKIATLTDKPEGRVVEIAADYTCFTIPEFVVGCLDYKENYRNLPYIGVKE 175

RESULT 14

ABU02782	ABU02782 standard; Protein; 180 AA.
XX	AC ABU02782;
XX	DT 11-FEB-2003 (first entry)

S. pneumoniae type 4 strain protein from coding region #2362.

XX	Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibiotic; immunostimulant; auditory; respiratory; gene therapy; vaccine.
XX	OS Streptococcus pneumoniae type 4 strain.
PN	WO200277021-A2.
XX	PD 03-OCT-2002.
XX	PF 27-MAR-2002; 2002WO-1B02163.
XX	PR 27-MAR-2001; 2001GB-0007658.
XX	PA (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
XX	PI Massignani V, Tettelein H, Fraser C;
XX	DR 2003-040579/03.
DR	N-PSDB; ABX08074.

XX	New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcal bacteria, such as pneumonia, sepsis, otitis media or ear infection.
XX	Claim 1; SEQ ID No 4724; 56pp; English.

CC The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as AB56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcal bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence.

CC Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

CC Sequence 180 AA;

Query	DLEYVLIPHGIIVDRIBLAKIMKDGYSDIMVLCKLGGKFKCADLVEHARNTSNSD 90
Db	5 DIKKVLVSHDETEAAKLGQLTKDYAGKNTLVLGKGSIPPEMAELVKHI-----D 57
Qy	91 RFVSMKVYDFIRLKSYRNDQSMGEMQIIGGGDLSLTLAKRNFLIVEDVYGTGRTMKALLSNI 150
Db	58 THIEM- DFMVMTSSYRGTASSGVINIKQDVTQDIKEFVQTLKNDRMF 115
Qy	151 EKYKPNMVKAVSLLVKRTSRSDGFRPDYAGFELPHLFLVGVYALDNEYFDRDLNHCYINE 210
Db	116 KEREAAVSVKIATLTDKPEGRVVEIAADYTCFTIPEFVVGCLDYKENYRNLPYIGVKE 175

SQ Sequence 180 AA;

Query Match 22.2%; Score 247.5; DB 24; Length 180;

Best Local Similarity 32.2%; Pred. No. 4.1e-19; Gaps 2;

Matches 58; Conservative 38; Mismatches 75; Indels 9; Gaps 2;

31 DLEYVLIPHGIIVDRIBLAKIMKDGYSDIMVLCKLGGKFKCADLVEHARNTSNSD 90

5 DIKKVLVSHDETEAAKLGQLTKDYAGKNTLVLGKGSIPPEMAELVKHI-----D 57

91 RFVSMKVYDFIRLKSYRNDQSMGEMQIIGGGDLSLTLAKRNFLIVEDVYGTGRTMKALLSNI 150

58 THIEM- DFMVMTSSYRGTASSGVINIKQDVTQDIKEFVQTLKNDRMF 115

151 EKYKPNMVKAVSLLVKRTSRSDGFRPDYAGFELPHLFLVGVYALDNEYFDRDLNHCYINE 210

OS KEREAAVSVKIATLTDKPEGRVVEIAADYTCFTIPEFVVGCLDYKENYRNLPYIGVKE 175

XX Sequence 180 AA;

Query	DLEYVLIPHGIIVDRIBLAKIMKDGYSDIMVLCKLGGKFKCADLVEHARNTSNSD 90
Db	5 DIKKVLVSHDETEAAKLGQLTKDYAGKNTLVLGKGSIPPEMAELVKHI-----D 57
Qy	91 RFVSMKVYDFIRLKSYRNDQSMGEMQIIGGGDLSLTLAKRNFLIVEDVYGTGRTMKALLSNI 150
Db	58 THIEM- DFMVMTSSYRGTASSGVINIKQDVTQDIKEFVQTLKNDRMF 115
Qy	151 EKYKPNMVKAVSLLVKRTSRSDGFRPDYAGFELPHLFLVGVYALDNEYFDRDLNHCYINE 210
Db	116 KEREAAVSVKIATLTDKPEGRVVEIAADYTCFTIPEFVVGCLDYKENYRNLPYIGVKE 175

SQ Sequence 180 AA;

Query Match 22.2%; Score 247.5; DB 24; Length 180;

Best Local Similarity 32.2%; Pred. No. 4.1e-19; Gaps 2;

Matches 58; Conservative 38; Mismatches 75; Indels 9; Gaps 2;

31 DLEYVLIPHGIIVDRIBLAKIMKDGYSDIMVLCKLGGKFKCADLVEHARNTSNSD 90

5 DIKKVLVSHDETEAAKLGQLTKDYAGKNTLVLGKGSIPPEMAELVKHI-----D 57

91 RFVSMKVYDFIRLKSYRNDQSMGEMQIIGGGDLSLTLAKRNFLIVEDVYGTGRTMKALLSNI 150

58 THIEM- DFMVMTSSYRGTASSGVINIKQDVTQDIKEFVQTLKNDRMF 115

151 EKYKPNMVKAVSLLVKRTSRSDGFRPDYAGFELPHLFLVGVYALDNEYFDRDLNHCYINE 210

OS KEREAAVSVKIATLTDKPEGRVVEIAADYTCFTIPEFVVGCLDYKENYRNLPYIGVKE 175

XX Sequence 180 AA;

RESULT 15

AAM01114

ID AAM01114 standard; Protein; 180 AA.

XX XX

AC AAM01114;

XX XX

DT 02-OCT-2001 (first entry)

XX XX

DE CFE 117 protein sequence.

XX XX

KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection;

KW KW antibiotic resistance.

XX XX

Streptococcus pneumoniae.

OS OS

XX XX

PT PT

WO200149721-A2.

XX XX

PD 12-JUL-2001.

XX XX

PP 29-DEC-2000; 2000WO-US35604.

XX XX

PR 30-DEC-1999; 99US-0174089,
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA XX
 PI Doughterty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucocleri RE;
 PI Thanassi JA;
 XX DR WPI; 2001-486721/54.
 XX N-PSDB; AAH30813.

PT Nucleic acids encoding conserved essential genes involved in bacterial
 PT replication which are potential targets for the treatment of antibiotic
 PT resistant bacterial infections -

XX Claim 27; Page 380; 380PP; English.

XX The present invention relates to nucleic acids (AAH90701-AAH90918) encoding polypeptides (AAM01002-AAM0114), which are essential for the viability of a bacterial cell wall. The acronym CEG stands for "CEG For Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon, by integrating an exogenous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest (comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids also enable identification of targets suitable for the treatment of antibiotic resistant bacterial infections.

XX Sequence 180 AA;

Query Match Score 245.5; DB 22; Length 180;
 Best Local Similarity 32.2%; Pred. No. 6.8e-19;
 Matches 58; Conservative 37; Mismatches 76; Indels 9; Gaps 2;

Qy	31	DLBEVLIIPHGLIVDRERLARDIMKDIGYSDIMVLCVIKGKYKFCADLVEHLKNTRNSD	90
Db	5	DIKKVLYSHDETEAARKLGAQTKDYGAKNPLVGLKGSTPMEVLYKII-----D	57
Qy	91	RFVSMKVDFIRIKSYRNDQSMQIIGGGDLSTLAGKNFLIVEDVGTGTTMALLSNI	150
Db	58	THIEM-DFMVMSYHGGTASSGVINIKQDVTDQIGRHLVLFEDIDTGQTLKNLRDMP	115
Qy	151	EKYKPMNIKVASLLVKRTSRSDGFRPYAGFPIPHLFVVGAYLDNEYFRDLNHCIVNE	210
Db	116	KAREANSVKIATLIDKPEGRVVIEADYTCFTIPNEFTVGYLDKENYRNLPYIGVKE	175

Search completed: November 13, 2003, 15:05:01
 Job time : 41 secs

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 15:04:11 ; Search time 21 Seconds

427.138 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVIMDDWPGYDILN.....LDYNEYFRDLNHCIVNEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCUTS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	1069	95.8	225	4	US-09-786-240-4	Sequence 4, Appli	
2	772	69.2	218	1	US-08-644-272A-14	Sequence 14, Appli	
3	263.5	23.6	200	4	US-09-107-332A-6646	Sequence 4646, Appli	
4	190	17.0	178	4	US-09-134-001C-3318	Sequence 3318, Appli	
5	7	157	14.1	214	4	US-09-252-991A-10612	Sequence 30612, Appli
6	119	10.7	179	4	US-09-117-532A-5030	Sequence 5030, Appli	
7	96	8.6	182	4	US-08-920-003A-2	Sequence 2, Appli	
8	10	96	8.6	182	4	US-08-920-003A-4	Sequence 4, Appli
9	11	89	8.0	187	4	US-09-134-001C-4780	Sequence 4780, Appli
10	12	88.5	7.9	1028	4	US-09-328-552-5749	Sequence 5749, Appli
11	13	87	7.8	494	3	US-08-993-260-3	Sequence 3, Appli
12	14	87	7.8	892	1	US-07-977-434-12	Sequence 12, Appli
13	15	87	7.8	892	1	US-08-458-19-12	Sequence 12, Appli
14	16	87	7.8	892	5	BCT-US81-0035-12	Sequence 12, Appli
15	17	84.5	7.6	207	4	US-09-252-991A-17055	Sequence 17055, Appli
16	18	84.5	7.6	272	4	US-09-107-532A-598	Sequence 5898, Appli
17	19	82	7.3	834	3	US-09-252-991A-21321	Sequence 31321, Appli
18	20	78.5	7.0	415	4	US-09-134-001C-4797	Sequence 5077, Appli
19	21	78.5	7.0	419	4	US-09-328-552-6451	Sequence 6451, Appli
20	22	78.5	7.0	1038	4	US-09-1541-782-4	Sequence 4, Appli
21	23	78	7.0	1038	4	US-09-723-320-4	Sequence 4, Appli
22	24	78	7.0	503	4	US-09-252-991A-12777	Sequence 3277, Appli
23	25	77	6.9	1169	1	US-08-315-468-4	Sequence 4, Appli
24	26	77	6.9	1218	1	US-09-589-567-2	Sequence 2, Appli
25	27	75.5	6.8				

ALIGNMENTS

RESULT 1

US-09-786-240-4

; Sequence 4, Application US/09786240

; Patent No. 6558935

; GENERAL INFORMATION:

; APPLICANT: INCYTE PHARMACEUTICALS, INC.

; APPLICANT: TANG, Y. Tom

; APPLICANT: CORLEY, Neil C.J.

; APPLICANT: GUEGELB, Karl R.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: LAL, Preeti

; APPLICANT: YUE, Henry

; APPLICANT: AZIMZAI, Jennifer L.

; TITLE OF INVENTION: HUMAN TRANSPERASE PROTEINS

; CURRENT APPLICATION NUMBER: US/09/786,240

; PRIORITY APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/1133,642

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PERL Program

; SEQ ID NO 4

; LENGTH: 225

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6558935 1404963CD1

US-09-786-240-4

Query Match 95.8%; Score 1069; DB 4; Length: 225;

Best Local Similarity 98.5%; Pred. No. 1.8e-19; Mismatches 2; Indels 1; Gaps 0;

Matches 203; Conservative 7; Other 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GVVIMDDWPGYDLYNLTYPHYGGDLEYWVLPYHGTIVDRERLAKIMDGYSDMVLIC 66

Db 14 GVVIMDDWPGYDLYNLTYPQHYYGDLEYWVLPYHGTIVDRERLAKIMDGYSDMVLIC 73

Qy 67 VLKGSKYKFCADLVEHLKNTISRNSDRFVSMKDFIRLKSYRNQSMGEMOLIGGGDLSTLA 126

Db 74 VLKGSKYKFCADLVEHLKNTISRNSDRFVSMKDFIRLKSYRNQSMGEMOLIGGGPLSTLA 133

Qy 127 GKNFLIVEDVYGTGTRTMKALLSNIEKYKPNMKVIAASLYKRTSRSDGFRDYAGFEIPIHL 186

Db 134 GKNFLIVEDVYGTGTRTMKALLSNIEKYKPNMKVIAASLYKRTSRSDGFRDYAGFEIPIHL 193

Qy 187 FVVGALDNEYFRDLNHCIVNHBG 212

Db 194 FVVGALDNEYFRDLNHCIVNHBG 219

RESULT 2
 US-08-644-664-B-14
 Sequence 14, Application US/08644664B
 Patent No. 5776746
 GENERAL INFORMATION:
 APPLICANT: Denney, Jr., Dan W.
 TITLE OF INVENTION: Gene Application Methods
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Medien & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 ZIP: 94104
 COUNTRY: United States Of America

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,277A
 FILING DATE: 06-DEC-1996
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/644,664
 FILING DATE: 01-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Macknight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: GENITOPE-024406
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-761-277A-14

Query Match 69.2%; Score 772; DB 2; Length 218;
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 69.2%; Score 772; DB 1; Length 218;
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 61 DIMVLCVLRGGYKFCADLVEHLKNISNSDRFVSMKVDIYRKLKSYRNDQSMGEMQIIGGG 120
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 61 MATRSPGVVIMDDWPGYDNLTFPQHYYGDLBYVLIPHGTIVDRIBRLARDIMKDIGYS 60
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 61 DISTLAKNELLIVEDVGTGRTMKALLSNIEKPKNMIVKASLLVKRTSRSDGFRPDYAG 180
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 61 DIMVLCVLRGGYKFCADLVEHLKNISNSDRFVSMKVDIYRKLKSYRNDQSMGEMQIIGGG 120
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 61 HIVALCVLRGGYKFCADLVEHLKNISNSDRFVSMKVDIYRKLKSYRNDQSMGEMQIIGGG 180
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 61 DISTLAKNELLIVEDVGTGRTMKALLSNIEKPKNMIVKASLLVKRTSRSDGFRPDYAG 180
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 181 FEIPHLFVGVGALDYNEXYFRDLNHCYNEHG 212
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

Query Match 181 FEIPDKFVGVGALDYNEXYFRNLNHCYNEHG 212
 Best Local Similarity 67.9%; Pred. No. 5.3e-84;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-644-664-B-14

RESULT 3
 US-08-761-277A-14
 Sequence 14, Application US/08761277A
 GENERAL INFORMATION:
 APPLICANT: Denney, Jr., Dan W.
 TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Medien & Carroll, LLP

SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Anineillo, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCUMENT NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4646:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 00 amino acids
 TYPE: amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...200
 SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

Query Match 23.6%; Score 263.5; DB 4; Length 200;
 Best Local Similarity 38.1%; Pred. No. 2,6e-23;
 Matches 69; Conservative 39; Mismatches 58; Indels 15; Gaps 7;

Query 31 DLEYVLIPIHGIIIVDIERLAKDIMKDGYSDIMVLCYLGKFKCADLVEHLKNISRNSD 90
 Db 24 DIERILISQEIQVRCLEKGLKELTEIYQNPLVPLVKGAVPNA DIV-----RSID 76
 Qy 91 RFVSMKVDFIIRLKSYRN-DQMGEMQIGGDLST-LAGKFLIVEDVGTGRTMKALLS 148
 Db 77 TY- -LELDFMIVDSSYGNATVSSGEVKV- -KDLDTINVEGRLLIVEDIISGRT- RAYLN 131
 Qy 149 NIEKYY-KPMNIVKVASLIVKVRKRSRSDGFRPDYAGFEIPLHFLVYGAIDYNEFDRDLNHCY 207
 Db 132 DLFYRKAKSRSKIVTLLDKRGRVNVIEADYGVNPNEFVYGYGLDAAVRLNPIYG 191
 Qy 208 I 208
 Db 192 L 192

RESULT 5
 US-09-134-001C-3318
 / Sequence 33:8, Application US/09134001C
 / Patent No. 6380370
 / GENERAL INFORMATION:
 / APPLICANT: Lynn Doucette-Stamm et al
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 / FILE REFERENCE: GTC-007
 / CURRENT APPLICATION NUMBER: US/09/134,001C
 / CURRENT FILING DATE: 1998-08-13
 / PRIOR APPLICATION NUMBER: US 60/064,964
 / PRIOR FILING DATE: 1997-11-08
 / PRIOR APPLICATION NUMBER: US 60/055,779
 / NUMBER OF SEQ ID NOS: 5674
 / LENGTH: 181
 / TYPE: PRT
 / ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3318

Query Match 21.4%; Score 238.5; DB 4; Length 181;
 Best Local Similarity 33.5%; Pred. No. 2,2e-20;
 Matches 62; Conservative 38; Mismatches 56; Indels 29; Gaps 7;

Qy 31 DLEYVLIPIHGIIIVDIERLAKDIMKDGYSDIMVLCY- -YLKGGYKFCADLVEHL 82
 Db 6 DLKVNVLDS-----EDIQNICKENGAIIDYKDRPLVCGILKGSVMFNAIDLKRI 57
 Qy 83 KNTISRNDSRFVSMKVDFIIRLKSYR- -NDSQMGEMQIGGDL- -STLAGKFLIVEDVYGTG 140
 Db 58 D-----TSIDPNDVSSYHGGTTESTGVQIL- -KDLGASINENQDVLIEDILGTG 106
 Qy 141 RTMKALLSNIKEYKPKNMIVKASLVLKRTSRSDGFRPDYAGFEIPLHFLVYGAIDYNEFVR 200
 Db 107 TILKSTTELLQSRKVNSLEIATLIDKPNRRAKIEARYVGKKIPDEFVYGYGLDRESYR 166
 Qy 201 DINHI 205
 Db 167 NLPYI 171

RESULT 6
 US-09-328-352-4965
 / Sequence 4965, Application US/09328352
 / Patent No. 6562958
 / GENERAL INFORMATION:
 / APPLICANT: Gary L. Breton et al.
 / TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 / TITLE OF INVENTION: BAUMANNII FOR AMINO ACID AND NUCLEIC ACID SEQUENCES RELATING TO ACINETOBACTER
 / FILE REFERENCE: GTC99-03PA
 / CURRENT APPLICATION NUMBER: US/09/328,352
 / CURRENT FILING DATE: 1999-06-04
 / NUMBER OF SEQ ID NOS: 8225
 / SEQ ID NO. 4965
 / LENGTH: 178
 / TYPE: PRT
 / ORGANISM: Acinetobacter baumannii
 US-09-328-352-4965

Query Match 27.0%; Score 190; DB 4; Length 178;
 Best Local Similarity 26.0%; Pred. No. 1,3e-14;
 Matches 50; Conservative 44; Mismatches 60; Indels 38; Gaps 6;

Qy 35 VLPHGIIIVDIERLAKDIMKDGYSD- -INVLCKVYKFKCADLVEHLKNISRNSD 92
 Db 10 IMISTEIQVAKYKELQBQINSHYANSKDELVILGIRGSVFMADDL--CRITIKH- - 64
 Qy 93 VSMKVDFIIRLKSYRN-DQMGEMQIGGDLST-----LAGKFLIVEDVGTGRTMKALLS 148
 Db 65 -----LDFMTVSSY-----GGGTTSRDRVYLKLDLGEIGKDVVEEDIDSG 108
 Qy 141 RTMKALLSNIKEYKPKNMIVKASLVLKRTSRSDGFRPDYAGFEIPLHFLVYGAIDYNEFVR 200
 Db 109 NTLSKQVEMQTRPNSIQLCTLYSPRSRREIDLEVFLGFEEVEDKIVGYGLDQKYSR 168
 Qy 201 DLNHCVINEHG 212
 Db 169 ---HLFIGEIG 177

RESULT 7
 US-09-252-991A-30612
 / Sequence 30612, Application US/09252991A
 / Patent No. 6551795
 / GENERAL INFORMATION:
 / APPLICANT: Marc J. Rubenstein et al.
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 / FILE REFERENCE: 107196..136
 / CURRENT APPLICATION NUMBER: US/09/252,991A
 / CURRENT FILING DATE: 1999-02-18
 / PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 30612
 LENGTH: 214
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 3-09-252-991A-30612

Query Match 14.1%; Score 157; DB 4; Length 214;
 Best Local Similarity 26.2%; Pred. No. 1.6e-10;
 Matches 42; Conservative 36; Mismatches 66; Indels 16; Gaps 4;

46 IERLAKDIMKDIGSDIMIVLKVKGKPFCAVLVHLKNIRSNSDRFV 94
 57 IGRVAEAINRDLGETNPVFFCVMNGGLPSGKLLPLLD-----FPLELSYLHATR 107

106 RNDOSMGEMQIIGGDLSTLAGKNFLIVEDVGGTRTMKALLSNIKYPNMIKVASILV 165
 108 RNETSGGELFWRAKPEISPI-DRVLIDDEGTISAIIDFCKHAGARAVHTAVL 166

166 KRTSRSDGFRPD---YAGFEIPLFLVYGYALDNEYFRD 201
 167 KEHERK-APDLKASFTCGLYCAKDRYVFGYGMDFKGYMRN 204

RESULT 8
 Sequence 5030, Application US/09107532A
 Patent No. 6583375

GENERAL INFORMATION:
 APPLICANT: Lynn A. Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 PRIOR FILING DATE: 30-Jun-1998
 PRIORITY NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-8277
 TELEFAX: (781)893-82007
 INFORMATION FOR SEQ ID NO: 5030:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 179 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: *Enterococcus faecium*
 FEATURE:

NAME/KEY: misc-feature
 LOCATION: (B) LOCATION 1..179
 SEQUENCE DESCRIPTION: SEQ ID NO: 5030:
 US-09-107-532A-5030

Query Match 10.7%; Score 119; DB 4; Length 179;
 Best Local Similarity 25.5%; Pred. No. 4.1e-06;
 Matches 39; Conservative 37; Mismatches 61; Indels 16; Gaps 7;

QY 42 IVDRIT----ERLAKDIMKDIGSDIMIVLKVKGKPFCAVLVHLKNIRSNSDRFV 94
 Db 6 VVDQYMKRALKTRTYEELRNHSIQDIVLGKTRGTYIASRAERKQLED----ID 60

QY 95 MKYDFIRLKSYRNQSMG-EMQ1GGGDLIS-TLAGKNFLIVEDVGGTRTMKALLSNIK 152
 Db 61 IPVGBLDITLYRDKKENDEPELHS1PVSLEGKEVILDDVLYTGRIRAAAMDAMD 120

QY 153 Y-KPNM1KVASILYKRTSRSDGFRPDYAGEFIP 184
 Db 121 FGRPRKISLA-VLVDRGHRELPIRADYVGKNI P 152

RESULT 9
 US-08-920-803A-2
 Sequence 2, Application US/08920803A
 Patent No. 6331410

GENERAL INFORMATION:
 APPLICANT: Burnham, Martin T.
 APPLICANT: Lonetto, Michael A.
 APPLICANT: Warne, Patrick V.
 TITLE OF INVENTION: NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESS: Dechert, Price & Rhoads
 STREET: 4000 Bell Atlantic Tower, 1717 Arch Street
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102-7793

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/920,803A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dickinson, Q. Todd
 REGISTRATION NUMBER: 28,354
 REFERENCE/DOCKET NUMBER: GM10086
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215/994-2252
 TELEFAX: 215/994-2222
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 182
 TYPE: amino acids
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-920-803A-2

Query Match 8.6%; Score 96; DB 4; Length 182;
 Best Local Similarity 25.8%; Pred. No. 0.0024;
 Matches 40; Conservative 36; Mismatches 71; Indels 8; Gaps 6;

QY 33 EYVLIPIHGIIIVDRIERLAKDMDIGSDIMIVLKVKGKPFCAVLVHLKNIRSNSDRF 92

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RESULT 11
US-09-134-001C-4780
; Sequence 4780, Application US/09134001C
; Patent No. 6,380,370
; GENERAL INFORMATION:
; APPLICANT: Lynn Boucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4780
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4780

Query Match 8.0%; Score 89; DB 4; Length 187;
Best Local Similarity 25.6%; Pred. No. 0.017; Mismatches 70; Indels 18; Gaps 6;
Matches 41; Conservative 31; Mismatches 70; Indels 18; Gaps 6;

Qy 33 EYVLIPHGIIVDRERLAKDIMK-DIGYSDDIMVLCVLGGYKFCADLVEHLKNISRNNSDR 91
Db 15 ERILDEAAIQTITRAHETLEYNKSTKDLVLL-----GIKTRGAFLAHRIQDKINSTE 69

Qy 92 FVSMKVDIFRLKSYRDQSMGEMQIIGGDLST-----LAGKNFLIVEDVVGTRGMKA 145
Db 70 QQLVPTGTDIIFHRDVD-----KVVQQAQDYAFDINNDINNKVVVIIIDDVLYTGRTVRA 125

Qy 146 LLSNIERY-KPMIKVASSLLVYKRTSRSDGFRDAGFEP 184
Db 126 SDAILLHTRPIKIGLAA-LVDRGHRBLPIRADFGKNIP 164

RESULT 12
US-09-328-352-5749
; Sequence 5749, Application US/09328352
; Patent No. 6,562,958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO: 5749
; LENGTH: 1028
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5749

Query Match 7.9%; Score 88.5; DB 4; Length 1028;
Best Local Similarity 21.0%; Pred. No. 0.27; Mismatches 61; Indels 25; Gaps 7;
Matches 34; Conservative 42; Mismatches 61; Indels 25; Gaps 7;

Qy 33 EYVLIPHGIIVDRERLAKDIMK-DIGYSDDIMVLCVLGGYKFCADLVEHLKNISRNNSDR 92
Db 594 ELDIAP-GVRAKSVTNNISRDLARSMSMASVVEVPGKPYIGIEV-----PNSARE 644

Qy 93 VSMKVDIFRLKSYRDQSMGEM-----QIIGGGDLSTLAGKNFLIVEDVVGTRGMKA 118
Db 645 MVRLLBELLTPAYRDP-SALISMAGMDISGNPVLTDLAKPHMLVAGTTGSSKSVAVNSM 704

Qy 146 LLSNIERY-KPMIKVASSLLVYKRTSRSDGFRDAGF-EIPHL 186
Db 705 LLSMLKYYKTPOLR-----DPKQFLANNDPHT 738

Query Match 8.6%; Score 96; DB 4; Length 182;
Best Local Similarity 25.8%; Pred. No. 0.0024; Mismatches 36; Indels 71; Gaps 6;
Matches 40; Conservative 36; MisMatches 71; Indels 8; Gaps 6;

Qy 33 EYVLIPHGIIVDRERLAKDIMK-DIGYSDDIMVLCVLGGYKFCADLVEHLKNISRNNSDR 92
Db 3 ERIMDDAIIQRTVRAHILENNGTNLNLIGIKTGEYLANRIO-KIHQEQRRI 61

Qy 93 VSMKVDIFRLKSYRDQSMGEMQIIGGDLSTLAGKNFLIVEDVVGTRGMKA 150
Db 62 PTGTFID---ITYFDDIEMSSLTTKDAIDDTDTDKVVIIDDVLYTGRTVASLDI 118

Qy 151 -EKVKPNMVKVASLLVYKRTSRSDGFRDAGFEP 184
Db 119 LLNARPIKIGLAA-LVDRGHRBLPIRADFGKNIP 152

```

RESULT 13
US-08-993-260-3

Sequence 3, Application US/0893260

Patent No. 6031089

GENERAL INFORMATION:

APPLICANT: Bienkowski, Michael J.

TITLE OF INVENTION: No. 60310891 Sequences of p56, a Proteins Which Title of Effects K-APP Channels

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pharmacia and Upjohn, Co., Intel. Prop. Law

STREET: (1920-32-LAW)

CITY: 301 Henrietta Street

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 49001

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,260

FILING DATE:

CLASSIFICATION:

NAME: Wootton, Thomas A.

REGISTRATION NUMBER: 35,004

REFERENCE/DOCKET NUMBER: 6092

TELECOMMUNICATION INFORMATION:

TELEPHONE: (616) 833-7914

TELEFAX: (616) 833-8897

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 494 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

US-08-993-260-3

Query Match 7.8%; Score 87; DB 3; Length 494;

Best Local Similarity 20.4%; Pred. No. 0.13; Gaps 13;

Matches 56; Conservative 38; Mismatches 84; Indels 96;

Qy 13 DWPGYDLNLFRTYPDHYGYDILEYVLIIPHGIVTIDRERLAKIMDKIGYSDIMVLCVLKGQY 72

Db 124 DW-YLLNLFLRWEY-----GISFLRLQMWREMEKF---MRRYKQAHY 166

Qy 73 KPCADLVEHL-----KNSRNS-----DRFVSMKYDFIRLKSYRNDSQM- 111

Db 167 AFSG--VEELLYSLGESTFVNMTQHSAEBSLQGVTORFIDDYVSAVLRASTGOSAAMP 224

Qy 112 ---GEMQITGQGDLISTLACKNLFIVEDV--VGTGRTMALLSNTEKYP----- 155

Db 225 AFAGAMSAGAQSLWNSVBEQGNKLVCSGLKLTKANVTHATVTSVTLISTEGKALYQVAY 284

Qy 156 -----NMIRKVASLILVKRTSRSD---GFRP-----D 177

Db 285 ENVGNNSSDDIVVIAITPFLDNDSSNLNTAGFHPPIDDVQGSFQOPTVSLVHGYLNSS 344

Qy 178 YAGFELPHFVFGYAL-DYNEYFRLNHCIVIN 209

Db 345 YFGFPDPKLFPPFANLTTDPPSFFCTLDNCPVN 378

RESULT 14
US-07-977-434-12

; Sequence 12, Application US/07377434

; Patent No. 5466591

GENERAL INFORMATION:

APPLICANT: Gelfand, David H.

APPLICANT: Abramson, Richard D.

TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: 7

SOFTWARE: Wordperfect 2.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/977,434

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 590,490

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 590,466

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 590,490

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 523,394

FILING DATE: 15-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 590,213

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 523,394

FILING DATE: 17-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 143,441

FILING DATE: 12-JAN-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 063,509

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US90/07641

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 585,471

FILING DATE: 20-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 455,611

FILING DATE: 22-DEC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 609,157

FILING DATE: 02-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 557,517

FILING DATE: 24-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Luann Cserz

REGISTRATION/DOCKET NUMBER: 31-822

REFERENCE/DOCKET NUMBER: Case No. 5466591 8753

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 814-2972

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 892 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
 US-07-977-434-12

Query Match Similarity 7.8%; Score 87; DB 1; Length 892;
 Best Local Similarity 20.7%; Pred. No. 0 33; Mismatches 41; Indels 58; Gaps 10;
 Matches 45; Conservative 41; Mismatches 73; Indels 58; Gaps 10;

Qy 29 YGDLEVLIPPHGIVLDRIERLAKDMDI-----GYSDIM 63
 Db 212 YNSLEVLKNNLTLERLRLLEDSEKDLQSTIELVLLDYLDPMDYBKDEIYRGYNPDK 271
 Qy 64 VLCVLKGYYKFC-----DLVHLKN---15RNSDBFVSMKVDFIRLKSYRNQSMG--- 112
 Db 272 LLKVLL-KYFSSSTIKELNQBKLEKEYLIVDNEKLKKLAAEIBKYKTFSTDTETSSL 330
 Qy 113 --EMQIIGGDLSTLAGRNFLIVEDVGTGTMKALLSNIERYKPMIKVASSLLVVRTS- 169
 Db 331 PFEAKLV-GISIISTMEGKAYVLPVSHFGAKNISKL---1DKFLKQIQLQEKDYNIVGQNL 386
 Qy 170 -----RSDFRFDYAGFELPHL-FVVGYALDYN 197
 Db 387 KFDYETFKSMGFSPN----VPHFDIMIAYLINPDE 418

RESULT 15
 US-09-819-12

Sequence 12. Application US/08458819
 Patent No. 5795762

GENERAL INFORMATION:
 APPLICANT: Gelfand, David H.
 ADDRESS: Abramson, Richard D.
 TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 STREET: 340 Hoffmann-La Roche Inc.
 CITY: Nutley
 STATE: New Jersey
 ZIP: 07110-1199

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7
 SOFTWARE: Wordperfect 2.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,819
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/977,434
 FILING DATE: 23-FEB-1993
 APPLICATION NUMBER: US 590,466
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,213
 FILING DATE: 12-JAN-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 523,394
 FILING DATE: 15-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 143,441
 FILING DATE: 12-JAN-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 063,509
 FILING DATE: 17-JUN-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 899,241
 FILING DATE: 22-AUG-1986
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 746,121
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US90/07641
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 585,471
 FILING DATE: 20-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 455,611
 FILING DATE: 22-DEC-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 609,157
 FILING DATE: 02-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 557,517
 FILING DATE: 24-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Luann Cserf
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2972
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 892 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-458-819-12

Query Match 7.8%; Score 87; DB 1; Length 892;
 Best Local Similarity 20.7%; Pred. No. 0 33; Mismatches 58; Gaps 10;
 Matches 45; Conservative 41; Mismatches 73; Indels 58; Gaps 10;

Qy 29 YGDLEVLIPPHGIVLDRIERLAKDMDI-----GYSDIM 63
 Db 212 YNSLEVLKNNLTLERLRLLEDSEKDLQSTIELVLLDYLDPMDYBKDEIYRGYNPDK 271
 Qy 64 VLCVLKGYYKFC-----DLVHLKN---15RNSDBFVSMKVDFIRLKSYRNQSMG--- 112
 Db 272 LLKVLL-KYFSSSTIKELNQBKLEKEYLIVDNEKLKKLAAEIBKYKTFSTDTETSSL 330
 Qy 113 --EMQIIGGDLSTLAGRNFLIVEDVGTGTMKALLSNIERYKPMIKVASSLLVVRTS- 169
 Db 331 PFEAKLV-GISIISTMEGKAYVLPVSHFGAKNISKL---1DKFLKQIQLQEKDYNIVGQNL 386
 Qy 170 -----RSDFRFDYAGFELPHL-FVVGYALDYN 197
 Db 387 KFDYETFKSMGFSPN----VPHFDIMIAYLINPDE 418

Search completed: November 13, 2003, 15:07:26
 Job time : 22 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 13, 2003, 15:06:27 ; Search time 30 Seconds
(without alignments)

Scoring table: BLOSUM62

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVVIMDDWPGYDNLNHCYVINEHG 212

Scoring table: Gapext 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/ptodata/2/pubpa/US07_PUBCOMB.pep:
 2: /cgn2_6/ptodata/2/pubpa/US07_PCT_News_PUB.pep:
 3: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pep:
 4: /cgn2_6/ptodata/2/pubpa/US05_NEW_PUB.pep:
 5: /cgn2_6/ptodata/2/pubpa/US04_NEW_PUB.pep:
 6: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB.pep:
 7: /cgn2_6/ptodata/2/pubpa/US08_NEW_PUB.pep:
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 12: /cgn2_6/ptodata/2/pubpa/US09_NEW_PUB.pep:
 13: /cgn2_6/ptodata/2/pubpa/US10_PUBCOMB.pep:
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 15: /cgn2_6/ptodata/2/pubpa/US10C_PUBCOMB.pep:
 16: /cgn2_6/ptodata/2/pubpa/US10C_NEW_PUB.pep:
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 18: /cgn2_6/ptodata/2/pubpa/US60_PUBCOMB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

US-09-189-833B-2

Sequence 2, Application US/09189833B
; Patent No. US200206539A1

APPLICANT: Bednarik et al.

TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2

CURRENT APPLICATION NUMBER: US/09/189, 833B

CURRENT FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: US 08/461,031

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: PCT/US94/11914

PRIOR FILING DATE: 1994-10-19

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 212

TYPE: PRT

ORGANISM: Homo sapiens

US-09-189-833B-2

SUMMARIES

Query Match Length DB ID Description

Result No. Score

1 1116 100.0 212 9 US-09-189-833B-2 Sequence 2, Application US/09-189-833B-2

2 1116 100.0 212 9 US-09-902-705-2 Sequence 2, Application US/09-902-705-2

3 1069 95.8 225 12 US-10-427-631-4 Sequence 4, Application US/10-427-631-4

4 786 70.4 218 9 US-09-189-833B-8 Sequence 8, Application US/09-189-833B-8

5 786 70.4 218 9 US-09-902-705-8 Sequence 8, Application US/09-902-705-8

6 779 69.8 218 9 US-09-189-833B-7 Sequence 7, Application US/09-189-833B-7

7 779 69.8 218 9 US-09-902-705-7 Sequence 7, Application US/09-902-705-7

8 772 69.2 218 10 US-09-664-664-4 Sequence 14, Application US/09-664-664-4

9 446.5 40.0 231 9 US-09-189-833B-9 Sequence 9, Application US/09-189-833B-9

10 446.5 40.0 231 9 US-09-902-705-9 Sequence 9, Application US/09-902-705-9

11 339 30.4 230 12 US-10-143-13 Sequence 13, Application US/10-143-13

12 251.5 22.5 194 10 US-09-738-626-6465 Sequence 6465, Application US/09-738-626-6465

13 233.5 20.9 186 15 US-10-156-761-12199 Sequence 12199, Application US/10-156-761-12199

14 222.5 19.9 210 9 US-09-189-833B-10 Sequence 10, Application US/09-189-833B-10

15 222.5 19.9 210 9 US-09-902-705-10 Sequence 10, Application US/09-902-705-10

56 13.2 192 15 US-10-102-806-776 Sequence 776, Application US/10-102-806-776

17 11.7 10.5 192 15 US-09-738-626-5283 Sequence 5283, Application US/10-156-661-14390

18 11.7 10.5 192 15 US-09-798-029-39 Sequence 39, Application US/09-798-029-39

19 9.9 8.9 160 9 US-09-798-029-40 Sequence 40, Application US/09-798-029-40

20 9.6 8.6 152 9 US-10-066-198-13-9 Sequence 139, Application US/10-066-198-13-9

21 8.7 7.8 494 12 US-10-066-203-13-9 Sequence 139, Application US/10-066-203-13-9

22 8.7 7.8 494 14 US-10-066-500-13-9 Sequence 139, Application US/10-066-500-13-9

23 8.7 7.8 494 15 US-10-066-796-13-9 Sequence 139, Application US/10-066-796-13-9

24 8.7 7.8 494 15 US-10-066-273-13-9 Sequence 139, Application US/10-066-273-13-9

25 8.7 7.8 494 15 US-10-066-494-13-9 Sequence 139, Application US/10-066-494-13-9

26 8.7 7.8 494 15 US-10-066-669-13-9 Sequence 139, Application US/10-066-669-13-9

27 8.7 7.8 494 15 US-10-066-211-13-9 Sequence 139, Application US/10-066-211-13-9

28 8.7 7.8 494 15 US-10-066-193-13-9 Sequence 139, Application US/10-066-193-13-9

29 8.7 7.8 494 15 US-10-066-739-13-9 Sequence 139, Application US/10-066-739-13-9

30 8.7 7.8 494 15 US-10-066-226-13-9 Sequence 139, Application US/10-066-226-13-9

31 86.5 7.5 208 12 US-10-319-799-53 Sequence 53, Application US/10-319-799-53

32 83.5 7.5 430 12 US-09-882-227-392 Sequence 392, Application US/09-882-227-392

33 83 7.4 307 12 US-10-032-201B-258 Sequence 258, Application US/10-032-201B-258

34 82 7.3 811 9 US-09-815-242-5571 Sequence 5571, Application US/09-815-242-5571

35 81.5 7.3 397 9 US-09-815-242-12881 Sequence 12881, Application US/09-815-242-12881

36 81.5 7.3 431 9 US-09-815-242-12856 Sequence 12856, Application US/09-815-242-12856

37 81.5 7.3 431 9 US-09-815-242-11875 Sequence 11875, Application US/09-815-242-11875

38 78 7.0 327 10 US-09-925-300-1372 Sequence 210, Application US/09-925-300-1372

39 78 7.0 451 10 US-09-989-920-210 Sequence 201, Application US/09-989-920-210

40 76 7.0 319 12 US-10-032-201B-201 Sequence 6776, Application US/10-032-201B-201

41 75.5 6.8 399 10 US-09-738-626-6776 Sequence 14011, Application US/09-738-626-6776

42 75 6.7 314 9 US-09-815-242-14011 Sequence 14011, Application US/09-815-242-14011

43 75 6.7 641 12 US-10-288-930-76 Sequence 22, Application US/10-288-930-76

44 75 6.7 2991 12 US-09-970-944-22 Sequence 22, Application US/09-970-944-22

45 75 6.7 4349 12 US-10-174-677-76 Sequence 22, Application US/10-174-677-76

ALIGNMENTS

Qy 181 FEIPHLFVGYALDYNEYFRLDNHICVINEHG 212
 Db 181 FEIPHLFVGYALDYNEYFRLDNHICVINEHG 212

RESULT 2
 US-09-902-705-2
 Sequence 2, Application US/0902705
 Patent No. US20020081695A1

GENERAL INFORMATION:
 APPLICANT: Bednarik et al.
 TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
 FILE REFERENCE: PF118P1C1
 CURRENT APPLICATION NUMBER: US/09/902,705
 CURRENT FILING DATE: 2001-07-12
 PRIOR FILING DATE: 1995-06-05
 PRIOR APPLICATION NUMBER: PCT/US94/11914
 PRIOR FILING DATE: 1994-10-19
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 212
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-902-705-2

Query Match 100.0%; Score: 11.16; DB: 9; Length: 212;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATRSPGVYIMDDWPGYDNLFTYPQHYYCDLEYVLIPIHGIVDRIERLAKDIMKDIGYS 60
 Db 1 MATRSPGVYIMDDWPGYDNLFTYPQHYYCDLEYVLIPIHGIVDRIERLAKDIMKDIGYS 60

RESULT 4
 US-09-189-833B-8
 Sequence 8, Application US/09189833B
 Patent No. US20020063393A1
 GENERAL INFORMATION:
 APPLICANT: Bednarik et al.
 TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
 FILE REFERENCE: PF118P1D1
 CURRENT APPLICATION NUMBER: US/09/189, 833B
 CURRENT FILING DATE: 1998-11-12
 PRIOR APPLICATION NUMBER: US 08/4461, 031
 PRIOR FILING DATE: 1995-06-05
 PRIOR APPLICATION NUMBER: PCT/US94/11914
 PRIOR FILING DATE: 1994-10-19
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 8
 LENGTH: 218
 TYPE: PRT
 ORGANISM: Cricetulus longicaudatus
 US-09-189-833B-8

Query Match 70.4%; Score: 786; DB: 9; Length: 218;
 Best Local Similarity 60.3%; Pred. No. 5.8e-19; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MATRSPGVYIMDDWPGYDNLFTYPQHYYCDLEYVLIPIHGIVDRIERLAKDIMKDIGYS 60
 Db 1 MATRSPGVYIMDDWPGYDNLFTYPQHYYCDLEYVLIPIHGIVDRIERLAKDIMKDIGYS 60

Qy 1 MATRSPGVYIMDDWPGYDNLFTYPQHYYCDLEYVLIPIHGIVDRIERLAKDIMKDIGYS 60
 Db 1 MATRSPGVYIMDDWPGYDNLFTYPQHYYCDLEYVLIPIHGIVDRIERLAKDIMKDIGYS 60

Qy 61 DIMVLCVLRGKGYKFCADLVLPHKNTSRNSDRFVSMKVDFTRLKSYRNDQSMGENQIIGGG 120
 Db 61 DIMVLCVLRGKGYKFCADLVLPHKNTSRNSDRFVSMKVDFTRLKSYRNDQSMGENQIIGGG 120

Qy 121 DLSTLAGKNLIVEVPGVGTGRTMALLSNTEKYKPNMKVASYLVRKTSRSDGFRPDYAG 180
 Db 121 DLSTLAGKNLIVEVPGVGTGRTMALLSNTEKYKPNMKVASYLVRKTSRSDGFRPDYAG 180

Qy 181 FEIPHLFVGYALDYNEYFRLDNHICVINEHG 212
 Db 181 FEIPHLFVGYALDYNEYFRLDNHICVINEHG 212

RESULT 3
 US-10-427-631-4
 Sequence 4, Application US/10427631
 Publication No. US20010175923A1

GENERAL INFORMATION:
 APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
 APPLICANT: CORLEY, Neil C.; GUEBLER, Karl J.;
 APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
 APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
 APPLICANT: AZIMZAI, Valda

TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
 FILE REFERENCE: PF-092-1 DIV

CURRENT APPLICATION NUMBER: US/10/427, 631
 CURRENT FILING DATE: 2003-04-29
 PRIOR APPLICATION NUMBER: US 09/786, 240
 PRIOR FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: PCT/US99/20989
 PRIOR FILING DATE: 1999-09-09
 PRIOR APPLICATION NUMBER: US 60/172, 220
 PRIOR FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: US 60/155, 248
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: US 60/133, 642
 NUMBER OF SEQ ID NOS: 33

Qy 121 DLSTLAGKNLIVEVPGVGTGRTMALLSNTEKYKPNMKVASYLVRKTSRSDGFRPDYAG 180
 Db 121 DLSTLAGKNLIVEVPGVGTGRTMALLSNTEKYKPNMKVASYLVRKTSRSDGFRPDYAG 180

Qy 181 FEIPHLFVGYALDYNEYFRLDNHICVINEHG 212
 Db 181 FEIPHLFVGYALDYNEYFRLDNHICVINEHG 212

RESULT 5
 US-09-902-705-8
 Sequence 8, Application US/0902705
 ; Patent No. US20020081695A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednarik et al.
 ; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
 ; FILE REFERENCE: PF138P1CL
 ; CURRENT APPLICATION NUMBER: US/09/902,705
 ; CURRENT FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: US 08/461,031
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US94/11914
 ; PRIOR FILING DATE: 1994-10-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Cricetulus longicaudatus
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Qy 61 DIMVLCVLIKGGYKFCADLVEHLKNISRNSDREVSMKVDFIRLKSYRNDSQSMGEMQIIGGG 120
 Db 61 HIVALCVLIKGGYKFCADLVEHLKNISRNSDREVSMKVDFIRLKSYRNDSQSMGEMQIIGGG 120
 Qy 121 DISTLAGKFLIVEDVGTGRTMKALLSNEKYKPNNMKVASSLLVVRTSRSDGFRPDYAG 180
 Db 121 DISTLAGKFLIVEDVGTGRTMKALLSNEKYKPNNMKVASSLLVVRTSRSDGFRPDYAG 180
 Qy 181 FEIPPHLFVVGYALDNEYFRDLNHCVINEHG 212
 Db 181 FEIPPHLFVVGYALDNEYFRDLNHCVINEHG 212

RESULT 6
 US-09-189-833B-7
 ; Sequence 7, Application US/0918933B
 ; Patent No. US20020065393A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednarik et al.
 ; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
 ; FILE REFERENCE: PF138P1D1
 ; CURRENT APPLICATION NUMBER: US/09/189,833B
 ; CURRENT FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: US 08/461,031
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US94/11914
 ; PRIOR FILING DATE: 1994-10-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Qy 1 MATRSPGVVIMDDWPGYDNLFTYPHQHYGLEYVLLPHGIVDRLERLAKDMDKIGYS 60
 Db 1 MATRSPGVVIMDDWPGYDNLFTYPHQHYGLEYVLLPHGIVDRLERLAKDMDKIGYS 60
 Qy 61 DIMVLCVLIKGGYKFCADLVEHLKNISRNSDREVSMKVDFIRLKSYRNDSQSMGEMQIIGGG 120
 Db 61 HIVALCVLIKGGYKFCADLVEHLKNISRNSDREVSMKVDFIRLKSYRNDSQSMGEMQIIGGG 120
 Qy 121 DISTLAGKFLIVEDVGTGRTMKALLSNEKYKPNNMKVASSLLVVRTSRSDGFRPDYAG 180
 Db 121 DISTLAGKFLIVEDVGTGRTMKALLSNEKYKPNNMKVASSLLVVRTSRSDGFRPDYAG 180
 Qy 181 FEIPPHLFVVGYALDNEYFRDLNHCVINEHG 212
 Db 181 FEIPPHLFVVGYALDNEYFRDLNHCVINEHG 212

RESULT 7
 US-09-902-705-7
 ; Sequence 7, Application US/09902705
 ; Patent No. US20020081695A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednarik et al.
 ; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
 ; FILE REFERENCE: PF138P1CL
 ; CURRENT APPLICATION NUMBER: US/09/902,705
 ; CURRENT FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: US 08/461,031
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US94/11914
 ; PRIOR FILING DATE: 1994-10-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Qy 1 MATRSPGVVIMDDWPGYDNLFTYPHQHYGLEYVLLPHGIVDRLERLAKDMDKIGYS 60
 Db 1 MATRSPGVVIMDDWPGYDNLFTYPHQHYGLEYVLLPHGIVDRLERLAKDMDKIGYS 60
 Qy 121 DISTLAGKFLIVEDVGTGRTMKALLSNEKYKPNNMKVASSLLVVRTSRSDGFRPDYAG 180
 Db 121 DISTLAGKFLIVEDVGTGRTMKALLSNEKYKPNNMKVASSLLVVRTSRSDGFRPDYAG 180
 Qy 181 FEIPPHLFVVGYALDNEYFRDLNHCVINEHG 212
 Db 181 FEIPPHLFVVGYALDNEYFRDLNHCVINEHG 212

RESULT 8
 US-09-925-664-14
 ; Sequence 14, Application US/09925664
 ; Patent No. US2002160006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Denney, Jr., Dan W.
 ; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
 ; FILE REFERENCE: GENITOPE-06499
 ; CURRENT APPLICATION NUMBER: US/09/925,664
 ; CURRENT FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 1999-08-09
 ; PRIOR FILING DATE: 1999-08-09
 ; PRIOR APPLICATION NUMBER: 1996-05-01
 ; PRIOR FILING DATE: 1996-05-01
 ; PRIOR APPLICATION NUMBER: 08/761,277
 ; PRIOR FILING DATE: 1996-12-06

Qy 1 MATRSPGVVIMDDWPGYDNLFTYPHQHYGLEYVLLPHGIVDRLERLAKDMDKIGYS 60
 Db 1 MATRSPGVVIMDDWPGYDNLFTYPHQHYGLEYVLLPHGIVDRLERLAKDMDKIGYS 60

RESULT 12
 US-09-738-626-6465
 ; Sequence 6465, Application US/09738626
 ; Publication No. US2002019765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SETKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SEQ ID NO: 6465
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-6465
 Query Match 22 5%; Score 251 5; DB 10; Length 194;
 Best Local Similarity 34.3%; Pred. No. 1e-19; Indels 23; Gaps 9;
 Matches 69; Conservative 41; Mismatches 68; Indexes 9;
 Qy 18 DLNLFTYPQHYG-DLEYVLIIPHGLIVDRERLAKDMDK1--GYSDDIVMLCVLKGYKF 74
 Db 6 D1N--PAPYGTGTDLESVNLSEKELKQRAEMAKRVESEFKDADLILVCLVKGAFYF 62
 Qy 75 CADLVEHLKNIISRSNDRFVNMKVDFTRLKSYRND-QSMGMQIIGGDLSTLAGKNFLIV 133
 Db 63 LAD----FSRMLD--ITPQSEPMAVSSYGNSTSSSGVRLKDKD--KBEIGRDVLIV 112
 Qy 134 EDVVGTRMALKALISNTEKYKPNMVKVASILVK--RTSSDGRPDYAGEFIPHLYVG 190
 Db 113 ED1DSGLTISWLMENLNQNPKSNVITLRLKPERLTTNIDMFD--1GFDIPNEFVYG 169
 Qy 191 YALDNEYFEDLNHICVINEH 211
 Db 170 YGLDFAEYRDLPYGTLEPH 190
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HIRAKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-274697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO: 12199
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 Query Match 20.9%; Score 233.5; DB 15; Length 186;
 Best Local Similarity 33.1%; Pred. No. 9.6e-18;
 Matches 61; Conservative 37; Mismatches 72; Indexes 13; Gaps 4;
 Qy 31 DLEYVLIIPHGLIVDRERLAKDMDK1GYSDDIVMLCVLKGYKFADLVEHLKNIISRNSD 90
 Db 11 DLKSVLITKEEIDAKAELAKAKIDAEYAGKDLILVGVLKGAVNMMLALARLS-----63
 Qy 91 RFVSMKVDIFTRLKSY-RNDGSMGEMQIIGGDLST-LAGKNFLIVEDVVGRTMALLS 148
 Db 64 --TPVIMDWWAVSSYGAQTQSGWVRL--KDLDTIKGKHVLIVEDDIDGTLISWLIS 119
 Qy 149 NIEKYPNMIKVASILVKYKPTSRSDGFRPDYAGEFIPHLYVGALDNEYFEDLNHICV1 208
 Db 120 NLGSRPASLKVCLTRKPEAKVAIDVWYGF1PNEFVIGYGLDIAEKYRNLPPVGTL 179
 Qy 209 NEH 211
 Db 180 APH 182
 RESULT 13
 US-09-189-833B-10
 ; Sequence 10, Application US/09189833B
 ; Patent No. US2002006539A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednarik et al.
 ; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
 ; FILE REFERENCE: EP13891D1
 ; CURRENT APPLICATION NUMBER: US/09/189,833B
 ; CURRENT FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: US 08/461,031
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US94/11914
 ; PRIOR FILING DATE: 1994-10-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 10
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Trypanosoma brucei
 US-09-189-833B-10
 Query Match 19.9%; Score 222.5; DB 9; Length 210;
 Best Local Similarity 29.3%; Pred. No. 1.9e-16;
 Matches 54; Conservative 46; Mismatches 65; Indexes 19; Gaps 5;
 Qy 35 VLPHGGIVDRIERLAKDMDK1GYSD-----IMVLCKVKGKFADLVEHLKNI 85
 Db 13 VLPHGGIVDRIERLAKDMDK1GYSD-----IMVLCKVKGKFADLVEHLKNI 85
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; SEQ ID NO: US20020119018A1
 ; Publication No. US20020119018A1
 ; NUMBER OF SEQ ID NOS: 144
 ; SEQ ID NO: 144
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Trypanosoma brucei
 US-09-189-833B-10
 Query Match 19.9%; Score 222.5; DB 9; Length 210;
 Best Local Similarity 29.3%; Pred. No. 1.9e-16;
 Matches 54; Conservative 46; Mismatches 65; Indexes 19; Gaps 5;
 Qy 35 VLPHGGIVDRIERLAKDMDK1GYSD-----IMVLCKVKGKFADLVEHLKNI 85
 Db 13 VLPHGGIVDRIERLAKDMDK1GYSD-----IMVLCKVKGKFADLVEHLKNI 85
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; SEQ ID NO: US20020119018A1
 ; Publication No. US20020119018A1
 ; NUMBER OF SEQ ID NOS: 144
 ; SEQ ID NO: 144
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Trypanosoma brucei
 US-09-189-833B-10
 Query Match 19.9%; Score 222.5; DB 9; Length 210;
 Best Local Similarity 29.3%; Pred. No. 1.9e-16;
 Matches 54; Conservative 46; Mismatches 65; Indexes 19; Gaps 5;

RESULT 15

US-09-902-705-10

Sequence 10, Application US/0902705

Patent No. US20020081695A1

GENERAL INFORMATION:

APPLICANT: Bednarik, et al.

TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2

FILE REFERENCE: PF138P1C1

CURRENT APPLICATION NUMBER: US/09/902,705

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US 08/461,031

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: PCT/US94/11914

PRIOR FILING DATE: 1994-10-19

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 210

TYPE: PRT

ORGANISM: Trypanosoma brucei

US-09-902-705-10

Query Match 19.0%; Score 222.5; DB 9; Length 210;

Best Local Similarity 29.3%; Pred. No. 1.9e-16;

Matches 54; Conservative 46; Mismatches 65; Indels 19; Gaps 5;

Qy 35 VLIPIGLIVDR1ERLAKMDIGSD-----IMVLcVTKGAYKFCADLVEHLKNI 85

Db 13 VLFTEELHMTMRGVAQRIADD-----YNCN1KPLLENLIVS1LKSSEFVFTADMVIL-- 67

Qy 86 SRNSDRFVSMKVDIFRLKSYRND-QSMGEMO1IGGDLSTLAGKFLIVEDVVGTCRTMK 144

Db 68 ---GDRGVPTRFELRASSYGHDTSGRVDKADG-LCDIGRKHVLVEDILDALTIR 123

Qy 145 ALLSNEKYKPNMIKYASLLAKRPTSSBDGFRDAGEFELPHIVGKAYALDNEYFRDLNH 204

Db 124 EVVDSLKSEPAKIKLVAIDKPGGRK1PFTAEEVVVADVPNVFVVGYGLDQSYREVRD 183

Qy 205 ICVI 208

Db 184 VVIL 187

Search completed: November 13, 2003, 15:11:49
 Job time : 31 secs

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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:03:26 ; Search time 20 Seconds

(without alignments)
1019.388 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1

Sequence: MATRSPGVYIMDDWPGYDNL.....LDNEYFRDLNHCIVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	786	70.4	218	S43043	hypoxanthine (guan
2	783	70.2	214	1 RTHUG	hypoxanthine Phosp
3	779	69.8	218	4 S21474	hypoxanthine Phosp
4	779	69.8	218	5 777	hypoxanthine Phosp
5	776	69.5	218	1 RTMSG	hypoxanthine Phosp
6	768	68.8	218	7 768	hypoxanthine Phosp
7	768	68.8	218	8 768	hypoxanthine Phosp
8	69.8	44.7	285	9 498.5	hypoxanthine Phosp
9	69.5	43.5	284	10 447.5	hypoxanthine Phosp
10	40.1	231	2	11 446.5	hypoxanthine Phosp
11	40.0	231	2	12 446.5	hypoxanthine Phosp
12	39.9	231	2	13 446.5	hypoxanthine Phosp
13	26.5	23.8	180	14 265.5	hypoxanthine Phosp
14	23.8	180	2	15 265.5	hypoxanthine Phosp
15	23.4	183	2	16 261	hypoxanthine Phosp
16	23.4	183	2	17 261	hypoxanthine Phosp
17	23.4	183	2	18 257.5	hypoxanthine Phosp
18	23.1	178	2	19 255	hypoxanthine Phosp
19	22.8	178	2	20 254.5	hypoxanthine Phosp
20	22.8	178	2	21 250.5	hypoxanthine Phosp
21	22.4	178	2	22 247.5	hypoxanthine Phosp
22	22.2	180	2	23 247.5	hypoxanthine Phosp
23	22.2	180	2	24 244.5	hypoxanthine Phosp
24	21.9	175	2	25 239.5	hypoxanthine Phosp
25	21.5	179	2	26 235.5	hypoxanthine Phosp
26	21.1	187	2	27 232.5	hypoxanthine Phosp
27	20.8	179	2	28 229	hypoxanthine Phosp
28	20.5	171	2	29 227.5	hypoxanthine Phosp

RESULT 1

S43043

hypoxanthine (guanine) phosphoribosyltransferase - long-tailed hamster

C;Species: Cricetulus longicaudatus (long-tailed hamster)

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 18-Jun-1999

C;Accession: S43043

R;Wei, S.J.C.; Chang, R.L.; Bachach, N.; Cui, X.X.; Merkler, K.A.; Wong, C.Q.; Hennig, Cancer Res., 53, 3294-3301, 1993

A;Title: Dose-dependent differences in the profile of mutations induced by (+)-7R, 8S-dihorribosyl transferase gene in Chinese hamster V-79 cells.

A;Reference number: S43043; PMID:8324741.

A;Accession: S43043

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-218 <WEI>

A;Cross-references: EMBL:X59652; NID:9461343; PID:CAA42198.1; PMID:9461344

C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 70.4%; Score 786; DB 2; Length 218;

Best Local Similarity 69.3%; Pred. No. 3.1e-59; Matches 147; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

Qy	1 MATRSPGVYIMDDWPGYDNLFTYPOHYGYDLEYVLIPHGTIVDRERLAKDIMKDIGYS 60
Db	1 MATRSPGVYIMDDWPGYDNLFTYPOHYGYDLEYVLIPHGTIVDRERLAKDIMKDIGYS 60
Qy	61 DIMWLCVKGKGYKECADLVEHLKMNISRSNDRFSYMSKVDIPLRKSYRNIDOSMGMQIIGGG 120
Db	61 HIALVCLVKGKGYKFADLIDYKALRNRSNDRSFLPMTDFIRLSYCNQDSTGDKVIGGD 120
Qy	121 DLSLQAGANFLIVEDVWGTGRTMKALLSITERYKPNMVKASLLVKKRSTSRSRSDGPRDAG 180
Db	121 DLSLQAGANFLIVEDVWGTGRTMKQMTLISVSKRNPVKYKVASLLVKKRSTSRSVGYRPRDFVG 180
Qy	181 FEIPHLFVGYALDNEYFRDLNHCIVINEHG 212
Db	181 FEIPHLFVGYALDNEYFRDLNHCIVINEHG 212

RESULT 2

I49758

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - western wild mouse (fragment)

C;Species: Mus spretus (western wild mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C;Accession: I49758

R;Johnson, G.G.; Kronert, W.A.; Bernstein, S.I.; Smith, K.D.

J. Biol. Chem., 263, 9019-9082, 1988

A;Title: Altered turnover of allelic variants of hypoxanthine phosphoribosyltransferase

A;Reference number: I49758; PMID:88243783; PMID:3319061

A;Accession: I49758

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

ALIGNMENTS

A;Residues: 1-214 <RES>
 A;Cross-references: GB:M20011; NID:9194000; PIDN:AAA6234.1; PID:g194001
 C;Keywords: glycosyltransferase; pentosyltransferase
 C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match Score 783; DB 2; Length 214;
 Best Local Similarity 68.9%; Pred. No. 5.4e-59;
 Matches 146; Conservative 31; N mismatches 35; Indels 0; Gaps 0;

A;Residues: 2-103, 'R', 105-218 <W13>
 A;Experimental source: variant Munich
 A;Note: this substitution is in the probable hypoxanthine-binding site and results in al
 R;Snyder, F.F.; Chudley, A.E.; MacLeod, P.M.; Carter, R.J.; Fung, E.; Lowe, J.K.
 Hum. Genet. 67, 18-22, 1984
 A;Title: Partial deficiency of hypoxanthine-guanine phosphoribosyltransferase with redu
 A;Reference number: 154249; MUID:84263016; PMID:6204922
 A;Accession: 154249
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-193, 'E', 195-218 <SNY>
 A;Cross-references: GB:L29387; NID:9459816; PIDN:AA59392.1; PID:9459817
 R;Lightfoot, T.; Joshi, R.; Nuki, G.; Snyder, F.F.
 Hum. Genet. 88, 695-696, 1992
 A;Title: The point mutation of hypoxanthine-guanine phosphoribosyltransferase (HPRT) in
 A;Reference number: 154263
 A;Accession: 154263
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-151, 'G', 53-218 <LIG>
 A;Cross-references: GB:L29382; NID:9459814; PIDN:AA59391.1; PID:9459815
 R;Yamada, Y.; Goto, H.; Ogasawara, N.
 Adv. Exp. Med. Biol. 309B, 121-124, 1991
 A;Title: Identification of two independent Japanese mutant HPRT genes using the PCR tec
 A;Reference number: 151843; MUID:92142870; PMID:1840476
 A;Accession: 151843
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 183-187, 'A', 189-193 <YAM1>
 A;Cross-references: GB:S79313; NID:9244377; PIDN:AA21289.1; PID:9244378
 A;Note: Point mutation from a patient with Lesh-Nyhan syndrome

QY 1 MATRSPGVVIMDDPFGYDNLFTFQHYGFLPIPHGIVTRERAKDMDIGYS 60
 Db 1 MATRSPVVIISDDEGYDLLFCFPHYEDLEKVPIDTERAVKEMGHH 60
 QY 61 DIMVLCVLRKGYKPCADLVEHLKNISRSNDRFVSMKVDFTRLKSYRNDSGMQIIGGG 120
 Db 61 HIVALCVLRKGYKPCADLVEHLKNISRSNDRFVSMKVDFTRLKSYCNDDGTDIKVIGGD 120
 QY 121 DLSTLAGRNFLIVEDVVGPTGRTMALLSNIEKVKPNNMIVASLLVKRTSPSDGPRPDYAG 180
 Db 121 DLSTLTKRNFLIVEDIDGKTMQTLSSLVKRTSRSGVGRDPYGS 180
 Qy 181 FEIPHLFWYQYALDDNEYFRLDNHICVTVNPHG 212
 Db 181 FEIPDKEVNGYALDDNEYFRLDNHVCVISTG 212

RESULT 3

RTHUG Human Phosphoribosyltransferase (EC 2.4.2.8) [validated] - human
 N;Alternate names: hypoxanthine-guanine phosphoribosyltransferase
 C;Species: Homo sapiens (man)
 C;Date: 17-Dec-1982 #sequence revision 08-Feb-1996 #text change 17-Mar-2000
 C;Accession: A32728; A91963; A92344; A93469; I54263; I51843; I64798; I64
 R;Edwards, A.; Voss, H.; Rice, P.; Civitello, A.; Stegemann, J.; Schwager, C.; Zimmerman
 Genetics 6, 593-608, 1980
 A;Title: Automated DNA sequencing of the human HPRT locus.
 A;Reference number: A32728; MUID:90256168; PMID:2341149
 A;Accession: A32728
 A;Molecule type: DNA
 A;Residues: 1-218 <EDW>
 A;Cross-references: GB:M26434; NID:9184369; PIDN:AAA36012.1; PID:g184370; GB:j00205; GB:
 R;Jolly, D.J.; Okayama, H.; Berg, P.; Esty, A.C.; Filipula, D.; Bohlen, P.; Johnson, G.G.
 Proc. Natl. Acad. Sci. U.S.A. 80, 477-481, 1983
 A;Title: Isolation and characterization of a full-length expressible cDNA for human hyp
 A;Reference number: A93963; MUID:83169681; PMID:6300847
 A;Accession: A93963
 A;Molecule type: mRNA
 A;Residues: 2-218 <JOL>
 A;Cross-references: GB:M31642; GB:J00205; GB:V00530; NID:9184349; PIDN:AA52690.1; PID:9
 A;Note: initiator Met not shown
 A;Title: Human hypoxanthine-guanine phosphoribosyltransferase. Complete amino acid seque
 A;Reference number: A92344; MUID:82265315; PMID:7107641
 A;Accession: A92344
 A;Molecule type: protein
 A;Residues: 2-218 <WIL>
 A;Note: 107-Asp was also found, presumably as a result of deamidation after translation
 R;Wilson, J.M.; Tarr, G.E.; Kelley, W.N.
 Proc. Natl. Acad. Sci. U.S.A. 80, 870-873, 1983
 A;Title: Human hypoxanthine (guanine) phosphoribosyltransferase: an amino acid substitut
 A;Reference number: A93983; MUID:83144031; PMID:6572373
 A;Accession: A93983
 A;Molecule type: protein
 A;Residues: 2-109, 'L', 111-218 <W12>
 A;Experimental source: variant London
 A;Note: this form was isolated from a patient with severe gout
 R;Wilson, J.M.; Kelley, W.N.
 J. Biol. Chem. 259, 27-30, 1984
 A;Title: Human hypoxanthine-guanine phosphoribosyltransferase. Structural alteration in
 A;Reference number: A92469; MUID:84161915; PMID:6706336
 A;Accession: A92469
 A;Molecule type: protein

Query Match Score 779; DB 1; Length 218;
 Best Local Similarity 68.4%; Pred. No. 1.2e-58;
 Matches 145; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVVIMDDPFGYDNLFTFQHYGFLPIPHGIVTRERAKDMDIGYS 60

A;Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
 A;Reference number: A93446; MUID:83090437; PMID:6234614
 A;Accession: A26218
 A;Molecule type: mRNA
 A;Residues: 2-200; 'N', 202-218 <KON>
 A;Cross-references: GB:J00423; NID:9193984; PIDN:AAA96232.1; PID:9309315
 A;Note: initiator Met not shown
 A;Note: this variant protein has enzymatic activity and its sequence is expected to be
 ine having no enzymatic activity
 C;Genetics:
 A;Introns: 9/3; 45/2; 106/3; 128/3; 134/3; 162/2; 178/1; 203/3
 C;Superfamily: hypoxanthine phosphoribosyltransferase
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 69.6%; Score 777; DB 1; Length 218;
 Best Local Similarity 68.4%; Pred. No. 1.8e-58;
 Matches 145; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVVMDWPQGYDLNLFTYPHYGGDLEYVLLPHGIIVDRERLAKDIMKDIGYS 60
 Db 1 MATRSPGVVMDWPQGYDLNLFTYPHYGGDLEYVLLPHGIIVDRERLAKDIMKDIGYS 60
 C;Species: Cricetulus longicaudatus (long-tailed hamster)
 C;Accession: S21474
 C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 18-Jun-1999
 C;Cross-references: EMBL: X17656; NID: g49514; PIDN: CAA35648.1; PMID: 949515
 A;Description: A Chinese hamster Hprt point mutation reverts to the wild-type sequence.
 A;Reference number: S21474
 A;Molecule type: mRNA
 A;Residues: 1-218 <ROS>
 C;Superfamily: hypoxanthine phosphoribosyltransferase
 C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 69.8%; Score 779; DB 2; Length 218;
 Best Local Similarity 68.9%; Pred. No. 1.2e-58;
 Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVVMDWPQGYDLNLFTYPHYGGDLEYVLLPHGIIVDRERLAKDIMKDIGYS 60
 Db 1 MATRSPGVVMDWPQGYDLNLFTYPHYGGDLEYVLLPHGIIVDRERLAKDIMKDIGYS 60
 C;Species: Cricetulus griseus (Chinese hamster)
 C;Accession: S14402; A26219; T58003; A00579
 C;Cross-references: EMBL: X17656; NID: g49514; PIDN: CAA35648.1; PMID: 949515
 A;Title: The Chinese hamster Hprt gene: restriction map, sequence analysis, and multip
 A;Accession: S14402
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-218 <ROS>
 A;Cross-references: EMBL: X53073; NID: g49505; PIDN: CAA37247.1; PID: 9817936
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1990
 R;Konacki, D.S.; Brennand, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
 A;Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
 A;Accession: A26219
 A;Molecule type: mRNA
 A;Residues: 2-218 <KON>
 A;Cross-references: GB:J00060; NID:9191112; PIDN:AAA36990.1; PID:9304515
 A;Note: initiator Met not shown
 A;Note: this variant protein has enzymatic activity and its sequence is expected to be
 ine having no enzymatic activity
 R;Fuscoe, J.C.; Zimmerman, L.J.; Fekete, A.; Setzer, R.W.; Rossiter, B.J.
 R;Melton, D.W.; Konacki, D.S.; Brennand, J.; Fuscoe, J.C.; Caskey, C.T.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2147-2151, 1984
 A;Title: Structure, expression, and mutation of the hypoxanthine phosphoribosyltransferase
 A;Accession: 149756; MUID: 84193967; PMID: 3226107
 A;Accession: 149756
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-218 <RES>
 A;Cross-references: GB:K01515; NID: g193994; PIDN: AAA998271.1; PID: 9387206
 R;Konacki, D.S.; Brennand, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
 Nucleic Acids Res. 10, 6763-6775, 1982
 A;Cross-references: GB: S46270; NID: g257049
 C;Genetics:

RESULT 4

S21474 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - long-tailed hamster
 N;Alternate names: hypoxanthine guanine phosphoribosyltransferase
 C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 18-Jun-1999
 C;Accession: S21474
 C;Cross-references: EMBL: X17656; NID: g49514; PIDN: CAA35648.1; PMID: 949515
 A;Description: A Chinese hamster Hprt point mutation reverts to the wild-type sequence.
 A;Reference number: S21474
 A;Molecule type: mRNA
 A;Residues: 1-218 <ROS>
 C;Superfamily: hypoxanthine phosphoribosyltransferase
 C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 69.8%; Score 779; DB 2; Length 218;
 Best Local Similarity 68.9%; Pred. No. 1.2e-58;
 Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVVMDWPQGYDLNLFTYPHYGGDLEYVLLPHGIIVDRERLAKDIMKDIGYS 60
 Db 1 MATRSPGVVMDWPQGYDLNLFTYPHYGGDLEYVLLPHGIIVDRERLAKDIMKDIGYS 60
 C;Species: Cricetulus griseus (Chinese hamster)
 C;Accession: S14402; A26219; T58003; A00579
 C;Cross-references: EMBL: X17656; NID: g49514; PIDN: CAA35648.1; PMID: 949515
 A;Title: The Chinese hamster Hprt gene: restriction map, sequence analysis, and multip
 A;Accession: S14402
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-218 <ROS>
 A;Cross-references: EMBL: X53073; NID: g49505; PIDN: CAA37247.1; PID: 9817936
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1990
 R;Konacki, D.S.; Brennand, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
 A;Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
 A;Accession: A26219
 A;Molecule type: mRNA
 A;Residues: 2-218 <KON>
 A;Cross-references: GB:J00060; NID:9191112; PIDN:AAA36990.1; PID:9304515
 A;Note: initiator Met not shown
 A;Note: this variant protein has enzymatic activity and its sequence is expected to be
 ine having no enzymatic activity
 R;Fuscoe, J.C.; Zimmerman, L.J.; Fekete, A.; Setzer, R.W.; Rossiter, B.J.
 R;Melton, D.W.; Konacki, D.S.; Brennand, J.; Fuscoe, J.C.; Caskey, C.T.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2147-2151, 1984
 A;Title: Structure, expression, and mutation of the hypoxanthine phosphoribosyltransferase
 A;Accession: 149756; MUID: 84193967; PMID: 3226107
 A;Accession: 149756
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 32-44 <RES>
 A;Cross-references: GB: S46270; NID: g257049
 C;Genetics:

RESULT 5

RTMG hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - mouse
 N;Alternate names: hypoxanthine-guanine phosphoribosyltransferase
 C;Species: Mus musculus (house mouse)
 C;Accession: 31-Dec-1989 #sequence revision 09-Aug-1997 #text_change 11-Jun-1999
 R;Melton, D.W.; Konacki, D.S.; Brennand, J.; Fuscoe, J.C.; Caskey, C.T.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2147-2151, 1984
 A;Title: Structure, expression, and mutation of the hypoxanthine phosphoribosyltransferase
 A;Accession: 149756; MUID: 84193967; PMID: 3226107
 A;Accession: 149756
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 32-44 <RES>

A;Gene: hppt
 A;Introns: 9/3; 45/2; 106/3; 128/3; 134/3; 162/2; 178/1; 203/3
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 69.5%; Score 776; DB 1;
 Best Local Similarity 68.9%; Pred. No. 2.1e-58;
 Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVVIMDDWPGYDNLFLTYPOHYCDLEYVLIPIGIVDRLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 60
 Db 1 MATRSPGVVIMDDWPGYDNLFLTYPOHYCDLEYVLIPIGIVDRLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 60
 Qy 61 DIMVLCVLRGGYKFCADLVEHLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 120
 .Db 61 HIVALCVLRGGYKFCADLVEHLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 120
 Qy 121 DLSTLAGKFLIVEDVUGTGRTMKALLSNLEYKPNMVKASLLVKTTSRGDFRPFYAG 180
 Db 121 DLSTLAGKFLIVEDDITGTMOTLSSLYKPNMVKASLLVKTTSRGDFRPFYAG 180
 Qy 181 FEIPPHFVVGYALDNEYFRLNHICVINEHG 212
 Db 181 FEIPDKFVVGYALDNEYFRLNHICVINEHG 212

RESULT 7
 15142 hypoxanthine phosphoribosyltransferase - rat
 C;Species: Rattus sp. (rat)
 C;Accession: 151842 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999
 R;Chiaverotti, T.A.; Battula, N.; Monnat, R.J.
 Adv. Exp. Med. Biol. 300B, 117-120, 1991
 A;Title: Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence analysis.
 A;Reference number: 15142; PMID:32142869; PMID:1781355
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Cross-references: GB:MG3983; NID:9204658; PIDN:AAA41350.1; PID:9204659
 R;Mittelstaedt, R.A.; Heilich, R.H.
 Mutat. Res. 311, 139-148, 1994
 A;Title: Analysis of *in vivo* mutation in exon 8 of the rat *hppt* gene.
 A;Reference number: 158008; PMID:505940; PMID:526167
 A;Accession: 158008
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 163-203 <RE2>
 A;Cross-references: EMBL:U06049; NID:9600482; PIDN:AAA56887.1; PID:g452580
 C;Genetics:
 A;Gene: hppt
 A;Introns: 1-218 <RE3>
 A;Cross-references: R:MG3983; NID:9204658; PIDN:AAA41350.1; PID:9204659
 C;Superfamily: hypoxanthine phosphoribosyltransferase; pentosyltransferase; salvage pathway
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 68.8%; Score 768; DB 2;
 Best Local Similarity 67.5%; Pred. No. 1e-57;
 Matches 143; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVVIMDDWPGYDNLFLTYPOHYCDLEYVLIPIGIVDRLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 60
 Db 1 MSTLSPSVVISDDEPGYDNLFLCTPNHYAEDLKVFPIPHGLIMDTERLARDVNMKGHH 60
 Qy 61 DIMVLCVLRGGYKFCADLVEHLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 120
 Db 61 HIVALCVLRGGYKFCADLVEHLKNSRNDRSIPMTVDFRLKSYRNDSMGEMQIIGGG 120
 Qy 121 DLSTLAGKFLIVEDVUGTGRTMKALLSNLEYKPNMVKASLLVKTTSRGDFRPFYAG 180
 Db 121 DLSTLAGKFLIVEDDITGTMOTLSSLYKPNMVKASLLVKTTSRGDFRPFYAG 180

RESULT 9
 15142 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (*Schistosoma mansoni*)
 C;Species: Schistosoma mansoni
 C;Accession: S09614 #sequence_revision 12-Feb-1993 #text_change 28-Apr-1993
 C;Cross-references: Craig III, S.P.; Muralidhar, M.G.; McKerrow, J.H.; Wang, C.C.
 Nucleic Acids Res. 17, 1635-1647, 1989
 A;Title: Evidence for a class of very small introns in the gene for hypoxanthine-guanine-
 A;Reference number: S09614; PMID:89160320; PMID:2701934
 A;Accession: S09614
 A;Molecule type: DNA
 A;Residues: 1-285 <RE4>
 A;Cross-references: EMBL:X13531
 A;Note: the authors did not translate the codons for residues 1-54

RESULT 8
 15140 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - rat
 N;Alternate names: hypoxanthine-guanine phosphoribosyltransferase
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
 C;Cross-references: 66/3; 102/3; 166/3; 188/3; 221/3; 238/1; 263/3
 C;Superfamily: hypoxanthine phosphoribosyltransferase; salvage pathway
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

185 KADFGFSIPLDHVVGSYSLDYNEIFRDLDDHCLVNDEG 222

RESULTS 13

Db: JN0085 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - malaria parasite (Plasmodium falciparum) trophocytote antigen 1C11-53; guanine phosphoribosyltransferase; tRNA synthetase; Plasmodium falciparum; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jun-2000

A;Reference: JN0085; A61515

R;Vasantha Kumar, G.; Davis Jr., R.L.; Sullivan, M.A.; Donahue, J.P.

Gene 91, 63-69, 1990

A;Title: Cloning and expression in Escherichia coli of a hypoxanthine-guanine phosphoribosyltransferase; Reference number: JN0085; MUID:90382639; PMID:2205541

A;Accession: JN0085

A;Molecule type: mRNA

A;Residues: 1-211 <PAS>

A;Cross-references: EMBL:X16279

R;Kidon, C.

Mol. Biochem. Parasitol. 29, 125-132, 1988

A;Title: Isolation and partial characterisation of a 26 kilodalton antigen from Plasmodium falciparum

A;Reference number: A61515; MUID:88318789; PMID:3045539

A;Accession: A61515

A;Molecule type: protein

A;Residues: 2-202 <KID>

C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 39.9% Score 445.5; DB 2; Length 231; Best Local Similarity 42.7%; Pred. No. 2.1e-30; Matches 93; Conservative 40; Mismatches 74; Indels 11; Gaps 3;

Db: 5 SPGV-----VIMDDWPGYDNLNLFYPOHYGDLLEYVLIIPHGIIVDRIERLAKDIMKD1 57

Db: 6 NPGAGENAFDVFVKDDGYDIDSENTPAHKYKLVKVNGVTKNRIKELAYDIKKVY 65

Db: 7 GYSDIMVLCVLLKGGYKECADLVEHLKNIISNDSRFYSMKV--DFTRILKSYRNDSGM 114

Db: 66 NNEEFHILCLLKGSRGFFTAJLKHLSRHNYSAVETSKPLFGEHYVVKSYCNDQSTGT 125

Db: 115 QIGGGDLSLTLAKGNFLIVEDVGGTGRTMALLSNLTKYKENMIKVASLLVKTSDGF 174

Db: 126 BIV-SEDLSCLKGKHLVIVEDIDTKTLVFKCEYLUKFEIKTKVIACLFLKRTPLWNGF 184

Db: 175 RPDYAGFEIIPHFLFVGSYALDNEYFRDLNHCIVCINHG 212

Db: 185 KADFGFSIPLDHVVGSYSLDYNEIFRDLDDHCLVNDEG 222

RESULTS 14

Db: S66098 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) hprt - Bacillus subtilis

N;Alternate names: hypoxanthine-guanine phosphoribosyltransferase hprt

C;Species: Bacillus subtilis

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C;Accession: S66098; E65442

DNA Res. 1, 1-14, 1994

A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome

A;Reference: S65967; MUID:905135; PMID:7584024

A;Molecule type: DNA

A;Residues: 1-180 <OGA>

A;Cross-references: EMBL:D26185; PID:BA05303.1; PID:9467457

A;Note: the nucleotide sequence was submitted to the EMBL database, December 1993

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertelli, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodat, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Gene: hprt

C;Superfamily: hypoxanthine phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 23.8%; Score 265.5; DB 2; Length 180; Best Local Similarity 35.4%; Pred. No. 2.7e-15; Matches 64; Conservative 38; Mismatches 66; Indels 13; Gaps 4;

Db: 31 DLEYVLIIPHGLIVDRIERLAKDIMKD1GYSIMVLC--VLRGGYKFCADLVEHLKNISRN 88

Db: 5 DIEKVLLSEEETQKVKELGABLTSS--YQQTFLPLAIGVLRGALPMAIDLKHI-----56

Db: 89 SDRFVSYKPMVKDPIRILKSYRNDO-SMGEMQIIGGGDLST-LAGKNEFLIVEDVNGTGRTMKAL 146

Db: 57 -DTYLM--DMDVSSYGNSTVSSGVKII--KDLSLTSVGRDILIEDIIDSGLTSLYL 111

Db: 147 LSNIKRYKPNMKVAKSLLVKTTSRSGFRRPDYAGPPIPHLVEVYFLDNEYFRDLNHC 206

Db: 112 VELFRYRKAISKIKVIVTLDKESGRK&DIKADFVGFFEVYDPAEVVGCLSYDABRYRNLPYIG 171

Db: 207 VI 208

Db: 172 VL 173

RESULT 15

Db: 860814 hypothetical protein hprt [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

R;Boilotin, A.; Wincker, P.; Mauger, S.; Jaiillon, O.; Weissenbach, J.; Ehrlich, Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: G66814

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-180 <STO>

A;Cross-references: GB:AE005176; PID:gi12724518; PID:AAK05617.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 23.8%; Score 265.5; DB 2; Length 180; Best Local Similarity 35.4%; Pred. No. 2.7e-15; Matches 64; Conservative 38; Mismatches 66; Indels 13; Gaps 4;

Db: 32 LEYVLIIPHGLIVDRIERLAKDIMKD1GYSIMVLC--VLRGGYKFCADLVEHLKNISRNSDR 91

Db: 5 LKEVFLTREQLAERVYKVEGRKPLVYGLKSIIMFVYDLSLTSVGRDILIEDIIDSGLTSLYL 56

Db: 92 FVSMKDFDPLKSY-RNDGSMGENQIIGGGDLSTLA-GRNFLIVEDVNGTGRTMKALLSN 149

Db: 57 -IDAEVDFMDVTSYGISSGEVRIL-KDLSTVYAHGRDILIVEDIDTNTLYLKKL 113

Qy 150 IEKYKPNMIKVASILVKERTSRSDGFRPDYAGFELPHLFVVGYALDYNBYFRDLNHCIVTN 209
Db 114 LTGRQAHESVKIISLLDKPSGRKVTDIDADYVGFSPDAFTVGVGIDYAERRQLPYIGIFN 173
Qy 210 E 210
Db 174 E 174

Search completed: November 13, 2003, 15:06:52
Job time : 21 secs

FT 134 134 MAGNESIUM (BY SIMILARITY).
 FT 213 213 MW; 8844851C8BG50EE8 CRC64;
 SQ 213 AA; 23950 AA;

Query Match 69.7%; Score 778; DB 1; Length 213;
 Best Local Similarity 68.7%; Pred. No. 5,6e-58;
 Matches 145; Conservative 31; Mismatches 35; Indels 0; Gaps 0;

Qy 2 ATRSPEGVIMDDWPGYDILNFTYPHQHYGDLKYLPHGIVTVDIERLAKD1MKDIGYSD 61
 Db 1 ATRSPEGVIMDDWPGYDILNFTYPHQHYGDLKYLPHGIVTVDIERLAKD1MKDIGYSD 61

Qy 62 IMVLCVLKGKPFADLVEHLKNTNSRNSDRFSVSKYDFFIRLKSYRNDSQMGEMQIIGGD 121
 Db 61 IVALCVLKGKPFADLVEHLKNTNSRNSDRFSVSKYDFFIRLKSYRNDSQMGEMQIIGGD 120

Qy 122 LSTLAGKNEFLIVEDVYGTGTRMKALLSNIKEYKPNMIVKAVSLVVKERTSRSDGFRPDYAGP 181
 Db 121 LSTLTKGNLIVEDDITDGKTMQTLLSLVLQVSPKMYVKAVALSVVKERTSRSVYRPDFVGF 180

Qy 182 EIPHLFVYQVGDYNEYFRDLNHCIVNEHG 212
 Db 181 EIPDKFVYQVGDYNEYFRDLNHCIVSETG 211

RESULT 2

HPRT_HUMAN STANDARD; PRT; 217 AA.
 AC P00492;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGprt)
 DB (HGprtase).
 GN HPRT OR HPRT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID 9606; RN [1];
 RP SEQUENCE.
 RX MEDLINE=82265815; PubMed=7107641;
 RA Wilson J.M., Tarr G.E., Mahoney W.C., Kelley W.N.;
 RT "Human hypoxanthine-guanine phosphoribosyltransferase. Complete amino
 acid sequence of the erythrocyte enzyme.";
 RL J. Biol. Chem. 257:10978-10985(1982).
 RN [2];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83169681; PubMed=6300847;
 RA Jolly D.J., Okuyama H., Berg P., Esty A.C., Filippula D., Bohlen P.,
 RA Johnson G.G., Shiveley J.E., Hunkapillar T., Friedmann T.;
 RT "Isolation and characterization of a full-length, expressible cDNA for
 RT human hypoxanthine phosphoribosyl transferase";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:477-481(1983).
 RN [3];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90256166; PubMed=2341119;
 RA Edwards A., Voss H., Rice P., Civitello A., Stegemann J.,
 RA Schwager C., Zimmermann J., Eiflie H., Caskey C.T., Ansorge W.;
 RT "Automated DNA sequencing of the human HPRT locus.";
 RL Genomics 6:593-608 (1990).
 RN [4];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strasberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemer C.M., Schulter G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Wilson J.M., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia R.M., Gay L.J., Gibbs R.A.,
 RA Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Madan A., Rodrigues S.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttierield Y.S.N., Krzywinski M.I., Skalski J., Myers R.M.,
 RA Schnetzer A., Schein J.E., Jones J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5];
 RP SEQUENCE OF 1-8 FROM N.A.
 RX MEDLINE=87064322; PubMed=3023844;
 RA Patel P.I., Franson P.E., Caskey C.T., Chinault A.C.;
 RT "Fine structure of the human hypoxanthine phosphoribosyltransferase
 RT gene";
 RA Eads J.C., Scapin G., Xu Y., Grubmeyer C., Sacchettini J.C.;
 RT "The crystal structure of human hypoxanthine-guanine
 RT phosphoribosyltransferase with bound GMP.";
 RL Mol. Cell. Biol. 6:393-403 (1986).
 RN [6];
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94320143; PubMed=44444;
 RA Eads J.C., Scapin G., Xu Y., Grubmeyer C., Sacchettini J.C.;
 RT "The crystal structure of human hypoxanthine-guanine
 RT phosphoribosyltransferase with bound GMP.";
 RL Mol. Cell. Biol. 14:325-344 (1994).
 RN [7];
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99087111; PubMed=10360366;
 RA Shi W., Li C.M., Tyller P.C., Grubmeyer C.,
 RA Schramm V.L., Almo S.C.;
 RA "The 2.0 Å structure of human hypoxanthine-guanine
 RT phosphoribosyltransferase in complex with a transition-state analog
 RT inhibitor";
 RL Nat. Struct. Biol. 6:588-593 (1999).
 RN [8];
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=99268335; PubMed=10338013;
 RA Balendiran G.K., Molina J.A., Xu Y., Torres-Martinez J., Stevens R.,
 RA Focia P.J., Eakin A.E., Sacchettini J.C., Craig S.P. III;
 RA "Ternary complex structure of human HPRTase PRPP, Mg²⁺, and the
 RT inhibitor HPP reveals the involvement of the flexible loop in
 RT substrate binding";
 RL Protein Sci. 8:1023-1031 (1999).
 RN [9];
 RP REVIEW ON VARIANTS.
 RX MEDLINE=93138539; PubMed=1487231;
 RA Sculley D.G., Dawson P.A., Bimmerston B.T., Gordon R.B.;
 RA "A review of the molecular basis of hypoxanthine-guanine
 RT phosphoribosyltransferase (HPRT) deficiency";
 RT "Molecular basis of hypoxanthine-guanine phosphoribosyltransferase (HPRT) deficiency";
 RL Hum. Genet. 90:195-207 (1992).
 RN [10];
 RP VARIANT TORONTO;
 RX MEDLINE=83213351; PubMed=6853490;
 RA Wilson J.M., Kobayashi R., Fox I.H., Kelley W.N.;
 RA "Human hypoxanthine-guanine phosphoribosyltransferase.";
 RL J. Biol. Chem. 258:6458-6460 (1983).
 RN [11];
 RP VARIANT KINSTON;
 RX MEDLINE=83213350; PubMed=6853716;
 RA Wilson J.M., Kelley W.N.;
 RT "Molecular basis of hypoxanthine-guanine phosphoribosyltransferase in a patient with the Jesch-Nyhan syndrome.";
 RT deficiency in a patient with the Jesch-Nyhan syndrome.";
 RL J. Clin. Invest. 71:1331-1335 (1983).
 RN [12];
 RP VARIANT LONDON;
 RX MEDLINE=83144011; PubMed=6853737;
 RA Wilson J.M., Tarr G.E., Kelley W.N.;
 RA "Human hypoxanthine-guanine phosphoribosyltransferase: an amino
 acid substitution in a mutant form of the enzyme isolated from a
 RT patient with gout";
 RT "Human hypoxanthine-guanine phosphoribosyltransferase: an amino
 acid substitution in a mutant form of the enzyme isolated from a
 RT patient with gout";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:870-873 (1983).
 RN

RP	VARIANT MUNICH.	RN [23]
RX	Medline=94161915; PubMed=67065936;	RP VARIANT ARLINGEN; DETROIT; NEW BRITON AND NEW HAVEN.
RA	Wilson J.M., Kelley W.N.;	RA MEDLINE=8329210; PubMed=273857;
RA	"Human hypoxanthine-guanine phosphoribosyltransferase. Structural alteration in a dysfunctional enzyme variant (HPRTMunich) isolated from a patient with gout."	RA Davidson B.L., Tarle S.A., Palella T.D., Kelley W.N.;
RT	gradient gel electrophoresis and direct sequencing using in vitro DNA amplification: HPRT Munich."	RT "Molecular basis of hypoxanthine-guanine phosphoribosyltransferase deficiency in ten subjects determined by direct sequencing of amplified transcripts.";
RL	Am. J. Hum. Genet. 42:726-734 (1988).	RT J. Clin. Invest. 84:1342-146 (1989).
RN	VARIANT MUNICH.	RN
RX	Medline=98118910; PubMed=335823;	Query Match 69.4%; Score 774; DB 1; Length 217;
RA	Carliello N.F., Scott J.K., Kat A.G., Thilly W.G., Kechavong P.;	Best Local Similarity 68.2%; Pred. No. 1.2e-57;
RT	"Resolution of missense mutant in human genomic DNA by denaturing gradient gel electrophoresis and direct sequencing using in vitro DNA amplification: HPRT Munich."	Matches 31; Mismatches 36; Indels 0; Caps 0;
RL	Am. J. Hum. Genet. 42:726-734 (1988).	Matches 144; Conservative 31;
RN	VARIANT FLINT.	Qy 2 ATRSPGVIMDDWPGYDNLFLTPQHYGYDLEYLIPHGIIYDRLRLLAKD1MDKDGYS 61
RP	Medline=98255878; PubMed=3384338;	Db 1 ATRSPGVISDDEPGYDLDLFCIPNHYAEDLERVFTPHGLIMDRTRLLARDVMKGHH 60
RX	Davidson B.L., Pashmforoush M., Kelly W.N., Palella T.D.;	Qy 62 IMVLCVKGKGFPCADLVEHLKGNNSDREVSMSMKVDFIRLKSYRNNDQSMGEMQI 1GGD 121
RA	"Genetic basis of hypoxanthine-guanine phosphoribosyltransferase deficiency in a patient with the Lesch-Nyhan syndrome (HPRTFlint).";	Db 61 IVALCVKGKGFPCADLVEHLKGNNSDREVSMSMKVDFIRLKSYCNDQSTGDIKVJGGDD 120
RT	Gene 63:331-338 (1988).	
RL	VARIANT MIDLAND.	Qy 122 LSTLAKRNFLIVEDVGTGRIMKALUNTYKPNMVKAVSLVVKRTSRSDGFRPYAGF 181
RP	Medline=98121497; PubMed=3266398;	Db 121 LSTLTKRNFLIVEDVGTGRIMQTLISLVRQYNPKVAVSLVVKRTPRSVGYKPDVGF 180
RX	Davidson B.L., Palella T.D., Kelley W.N.;	Qy 182 EIPHLFVGVYALDYNEXYFRDLNHCWINEHG 212
RA	"Human hypoxanthine-guanine phosphoribosyltransferase: a single nucleotide substitution in cDNA clones isolated from a patient with Lesch-Nyhan syndrome (HPRTMidland).";	Db 181 EIPDKFVVGTGALDYNEXYFRDLNHCWIVSETG 211
RN	VARIANT ANN ARBOR.	RESULT 3
RP	Medline=98212418; PubMed=2896620;	HPRT_MOUSE
RX	Ruijter S., Hidaka Y., Davidson B.L., Palella T.D., Kelley W.N.;	ID _HPRT_MOUSE
RA	"Identification of a single nucleotide change in a mutant gene for hypoxanthine-guanine phosphoribosyltransferase (HPRT Ann Arbor).";	AC P00433;
RT	Hum. Genet. 79:39-43 (1988).	DT 21-JUL-1986 (Rel. 01, Created)
RL	VARIANT LONDON.	DT 01-OCT-1996 (Rel. 34, Last sequence update)
RN	Medline=99067158; PubMed=3198771;	182 EIPHLFVGVYALDYNEXYFRDLNHCWINEHG 212
RP	Davidson B.L., Chan S.J., Wilson J.M., Kelley W.N., Palella T.D.;	DB Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGprt)
RX	"Hypoxanthine-guanine phosphoribosyltransferase. Generic evidence for identical mutations in two partially deficient subjects.";	DE (HGprtase) (HGRT B).
RA	J. Clin. Invest. 84:2164-2176 (1988).	DE (HGRT B).
RN	VARIANTS DIRRANBANDI AND YERONGA.	GN Mus musculus (Mouse).
RP	Medline=9158110; PubMed=314064;	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RX	Keough D.T., Gordon R.B., Detersey J., Emmerson B.T.;	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RA	"Biochemical basis of hypoxanthine-guanine phosphoribosyltransferase deficiency in nine families.";	NCBI_TaxID=10090;
RT	Acta Paediatr. Jpn. Overseas Ed. 31:303-313 (1989).	RN [1]
RT	"Molecular analysis of hypoxanthine-guanine phosphoribosyltransferase mutations in five unrelated Japanese patients.";	RN SEQUENCE FROM N.A.
RT	J. Inherit. Metab. Dis. 11:229-238 (1988).	RP MEDLINE=33090437; PubMed=6294614;
RL	VARIANTS JAPAN-1 AND JAPAN-2.	RA Konecki D.S., Bremland J., Fuscoe J.C., Caskey C.T., Chinault A.C.;
RN	Medline=9022326; PubMed=2572141.	RT "Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hamster: construction and sequence analysis of cDNA recombinants.";
RP	VARIANT ASHLVILLE.	RT Chinault A.C., Bremland J., Caskey C.T.;
RX	Medline=90079703; PubMed=2909537;	RT "Structure, expression, and mutation of the hypoxanthine-guanine phosphoribosyltransferase gene.";
RA	Davidson B.L., Pashmforoush M., Kelly W.N., Palella T.D.;	Proc. Natl. Acad. Sci. U.S.A. 81:2147-2151 (1984).
RT	"Human hypoxanthine-guanine phosphoribosyltransferase deficiency in a patient with gout (HPRTAshville).";	CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
RT	J. Biol. Chem. 264:520-525 (1989).	CC alpha-D-ribose 1-diphosphate.
RL	VARIANT YALE.	CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
RN	Medline=89093407; PubMed=2910902;	CC alpha-D-ribose 1-diphosphate.
RP	VARIANT YALE.	CC -!- PATHWAY: Purine salvage.
RX	Fujimori S., Davidson B.L., Kelley W.N., Palella T.D.;	CC -!- SUBUNIT: Homotetramer (By similarity).
RA	"Identification of a single nucleotide change in the hypoxanthine-guanine phosphoribosyltransferase gene (HPRTYale).";	CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
RT	J. Clin. Invest. 83:11-13 (1989).	CC -!- SIMILARITY: BELONGS TO THE PURINE PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
RL		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

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Genomics 9:247-256 (1991).

[2]

SEQUENCE FROM N.A.

RE

DR	InterPro; IPR005904; Hxn_Phspho trans.	DR	EMBL; AJ132697; CAB46657.1; -.
DR	InterPro; IPR00275; Pr/PY_rP-transf.	DR	DR; P00492; 1HNP.
DR	InterPro; IPR00036; PRTransferase.	DR	HSSP; IP005904; Hxn_Phspho trans.
DR	Pfam; PF0016; Ribosyltrnase; 1.	DR	InterPro; IPR002345; Pr/PY_rP-transf.
DR	TIGRFAMS; TIGR01203; HGPRTase; 1.	DR	InterPro; IPR0008346; PRTransferase.
DR	PROSITE; PS00103; PUR_TYR_PR_TRANSFER; 1.	DR	Pfam; PF00156; Ribosyltrnase; 1.
KW	Transferase; Glycosyltransferase; Purine salvage; Magnesium.	DR	TIGRFAMS; TIGR01203; HGPRTase; 1.
FT	METAL 134 134 MAGNESIUM (BY SIMILARITY).	DR	PROSITE; PS00103; PUR_PR_TRANSFER; 1.
FT	METAL 135 135 MAGNESIUM (BY SIMILARITY).	KW	Transferase; Glycosyltransferase; Purine salvage; Magnesium.
SEQUENCE	218 AA; 24477 MW; 26833FC1444FEE0B5E CRC64;	FT	METAL 134 134 MAGNESIUM (BY SIMILARITY).
Query Match	68.8%; Score 768; DB 1; Length 218;	FT	METAL 135 135 MAGNESIUM (BY SIMILARITY).
Best Local Similarity	67.5%; Pred. No. 3.9e-57;	SQ	SEQUENCE 218 AA; 24608 MW; 2228B84B0BAAF727 CRC64;
Matches	143; Conservative 33; Mismatches 36; Indels 0; Gaps 0;	Query Match	67.5%; Score 753; DB 1; Length 218;
Qy	1 MATRSPGVIMDDWPGYDNLNFTYPOHQYGDLEYVLIPHGIIVDRERLAKDMDKIGYS 60	Best Local Similarity	67.0%; Pred. No. 6.4e-56;
Db	1 MSLSPSVTISDDEPGYDLDLFCIPNHYADELEKVKIPIHGLMDTRBLARDWKMKGH 60	Matches	142; Conservative 32; Mismatches 38; Indels 0; Gaps 0;
Qy	61 DINVLCLVKIGGYKFCADLVEHKLNISRNNSDRFSMKYDFTRLKSYRNNDQSMGEMQIIGGG 120	Qy	1 MATRSPGVIMDDWPGYDNLNFTYPOHQYGDLEYVLIPHGIIVDRERLAKDMDKIGYS 60
Db	61 HIALVCVIGGYKFFADLVEHKLNISRNNSDRFSMKYDFTRLKSYRNNDQSMGEMQIIGGG 120	Db	1 MATHSPCIVGDDEQYDLDLFCIPKHYADDLEKVKIPIHGLMDTRBLARDWKMKGH 60
Qy	121 DISTLAGKFLIEVDTYVSTGRTMKALLSNIKEYKPNMVKAVASLKVRTSRSDGFRPDYAG 180	Qy	61 DINVLCLVKIGGYKFCADLVEHKLNISRNNSDRFSMKYDFTRLKSYRNNDQSMGEMQIIGGG 120
Db	121 DISTLGTRKVLIEDIIDGKTMQTLSSVQSPKMYKVASLKVRTSRSDGFRPDYAG 180	Db	61 HIALVCVIGGYKFFADLVEHKLNISRNNSDRFSMKYDFTRLKSYRNNDQSMGEMQIIGGG 120
Qy	181 FEPFLHFVGYALDYNNEYFEDLNLHCVINEHG 212	Qy	121 DISTLGTRKVLIEDIIDGKTMQTLSSVQSPKMYKVASLKVRTSRSDGFRPDYAG 180
Db	181 FEPFDKFVGYALDYNNEYFEDLNLHCVISESG 212	Qy	181 FEPFLHFVGYALDYNNEYFEDLNLHCVINEHG 212
Db	181 FEPFDKFVGYALDYNNEYFEDLNLHCVISESG 212	Db	181 FEPFDKFVGYALDYNNEYFEDLNLHCVISETG 212
RESULT 7		RESULT 8	
HPRT_CHICK	HPRT_CHICK STANDARD; PRT; 218 AA.	HPRT_SCHMA	HPRT_SCHMA STANDARD; PRT; 284 AA.
AC	Q9W719; 16-OCT-2001 (Rel. 40, Created)	AC	HP09383; 01-MAR-1989 (Rel. 10, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)	DT	01-MAR-1989 (Rel. 10, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)	DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Hypoxanthine-Guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)	DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)
DE	(HGPRTase).	DE	(HGPRTase).
GN	Gallus gallus (Chicken).	GN	HGPRT.
HPRT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS	Schistosoma mansoni (Blood fluke).
OS	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Strigeida; Schistosoma.
OC	Gallus.	OC	Schistosomatidae; Schistosoma.
OC	NCBI TaxID:9031;	OX	NCBI_TaxID=6183;
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RX	MEDLINE=99216494; PubMed=10198428;	RC	STRAIN=Puerto Rican;
RA	Fukagawa T., Hayward N., Yang J., Azzalin C., Griffin D., Stewart A.F., Brown W.; "The chicken HPRT gene: a counter selectable marker for the DT40 cell line," Nucleic Acids Res. 27:1966-1969 (1999).	RA	MEDLINE=88303321; PubMed=3136439;
RT	"The chicken HPRT gene: a counter selectable marker for the DT40 cell line," Nucleic Acids Res. 27:1966-1969 (1999).	RA	Craig S.P., McKerrow J.H., Newport G.N., Wang C.C.; "Analysis of cDNA encoding the hypoxanthine-guanine phosphoribosyltransferase (HGPRTase) of Schistosoma mansoni; a putative target for chemotherapy," Nucleic Acids Res. 16:7087-7101(1988).
RL	alpha-D-ribose 1-diphosphate.	RT	RT
CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.	RT	RT
CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.	RT	RT
CC	-!- PATHWAY: Purine salvage.	RT	RT
CC	-!- SUBUNIT: Homotetrramer (By similarity).	RL	Nucleic Acids Res. 17:1635-1647(1989).
CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic.	RX	-!- CATALYTIC ACTIVITY: IMP + diphosphate = Hypoxanthine + 5-phospho-alpha-D-ribose 1-diphosphate.
CC	-!- SIMILARITY: BELONGS TO THE PURINE/ PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.	CC	CC
CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.	CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.
CC	-!- PATHWAY: Purine salvage.	CC	-!- PATHWAY: Purine salvage.
CC	-!- SUBUNIT: Homotetramer (By similarity).	CC	-!- SUBUNIT: Homotetramer (By similarity).
CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic.	CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic.

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RESULT 9						
	HNGAR_PLAFG		STANDARD:	PRT:	231 AA.	
CC	ID HGXR_PLAFG					
CC	ID P20035;					
CC	AC 01-PBB-1991	(Rel. 17, Created)				
CC	DT 01-FEB-1991	(Rel. 17, Last sequence update)				
CC	DT 28-FEB-2003	(Rel. 41, Last annotation update)				
CC	DE (HGXPRT) (HGXPRTase) (HGXPRT).	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.-)				
CC	GN LACZ	Plasmid falciparum (isolate FCR 3 / Gambia).				
CC	OS Eukaryota	Plasmid				
CC	OX Alveolata	Plasmid				
CC	NCBI_TaxID=5838;	Plasmid				
RN	[1]	SEQUENCE FROM N. A.				
RP	MEDLINE-20045974; PubMed=2682528;					
RP	RA VasanthaKumar G., Davis R.L. Jr., Sullivan M.A., Donahue J.P.;					
RP	RT "Nucleotide sequence of cDNA clone for hypoxanthine-guanine phosphoribosyltransferase from Plasmodium falciparum." Nucleic Acids Res. 17:8382-8382 (1989).					
RN	[2]	SEQUENCE FROM N. A.				
RP	MEDLINE=30382619; PubMed=2205541.					

RA	Wasanthakumar G., Davis R.L. Jr., Sullivan M.A., Donahue J.P.;
RT	"Cloning and expression in <i>Escherichia coli</i> of a hypoxanthine-guanine phosphoribosyltransferase-encoding cDNA from <i>Plasmodium falciparum</i> ."
RT	Gene 91:63-69 (1990).
RL	[3]
RN	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RR	Medline=9364963; PubMed=10433633;
RA	Shi W., Li C.M., Tyler P.C., Furneaux R.H., Cahill S.M., Girvin M.E., Grubmeyer C., Schramm V.L., Almo S.C.;
RA	"The 2.0 A structure of malarial purine phosphoribosyltransferase in complex with a transition-state analogue inhibitor.";
RT	Biochemistry 38:3872-3880 (1999).
RL	-!- FUNCTION: WORKS WITH GUANINE, HYPOXANTHINE AND XANTHINE.
CC	-!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-alpha-D-ribose 1'-diphosphate.
CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1'-diphosphate.
CC	-!- CATALYTIC ACTIVITY: 5'-phospho-alpha-D-ribose 1'-diphosphate + xanthine = (9-D-ribofylxanthine)-5'-phosphate + phosphate.
CC	-!- PATHWAY: Purine salvage.
CC	-!- SUBUNIT: Homotrimer.
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.
CC	-!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR	EMBL: X16279; CRA34355; 1. -.
DR	PIR: S06601; S06601.
DR	PDB; ICJB; 18-AUG-99.
DR	InterPro: IPR005024; Hxn_phospho_trans.
DR	InterPro: IPR002375; Pr_py_rp_transf.
DR	InterPro: IPR000836; PRTransfase.
DR	PFam: PF00156; Ribosyltran; 1.
DR	TIGRFAMS; TIGR01203; HGPRTase; 1.
DR	PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR	TRANSFase; GlycosylTransferase; Purine salvage; Magnesium; 3D-structure.
DR	MAGNESIUM (BY SIMILARITY).
FT	NETAL 144 144 MAGNESIUM (BY SIMILARITY).
FT	NETAL 145 145 MAGNESIUM (BY SIMILARITY).
FT	TURN 7 7
FT	STRAND 8 9
FT	TURN 11 12
FT	STRAND 17 18
FT	TURN 21 22
FT	STRAND 25 25
FT	HELIX 27 29
FT	TURN 34 36
FT	HELIX 37 39
FT	STRAND 40 45
FT	HELIX 47 65
FT	TURN 66 67
FT	STRAND 70 76
FT	TURN 77 79
FT	HELIX 80 97
FT	TURN 100 101
FT	STRAND 106 117
FT	TURN 118 119
FT	STRAND 120 129
FT	HELIX 132 135
FT	STRAND 136 136
FT	TURN 137 137
FT	STRAND 139 147
FT	HELIX 151 160
FT	HELIX 161 163
FT	STRAND 165 165
FT	STRAND 167 167

PT	TURN	122	123
RA	HELIX	130	130
RA	HELIX	135	137
RA	TURN	138	139
RA	STRAND	141	149
RA	HELIX	153	163
RA	TURN	164	165
RA	STRAND	169	178
RA	TURN	183	184
RA	STRAND	187	187
RA	STRAND	190	195
RA	STRAND	200	202
RA	TURN	203	204
RA	STRAND	205	205
RA	TURN	208	213
RA	STRAND	217	219
RA	HELIX	222	226
RA	TURN	227	227
RA	SEQUENCE	230 AA;	26386 MW;
RA		C3784254BF96361D	CRC64;
RA	Query Match	31	0%
RA	Best Local Similarity	35	5%
RA	Matches	70;	Conservative
RA	Mismatches	49;	Indels
RA	Gaps	2	
RA	Qy	17	YDLNLTYPHYGDLLEYVLIIPHGGIVDRLERLADIMKIGYSIDIMVLCVLRGKFCFA
RA	Db	27	YNADDELVPHACKPKYIDKILLPGGLVKDRYKLAIDIHRYTFGEELHIICLKGSRGFFN
RA	RA	86	86
RA	Qy	77	DLVEHKLKNTRNSDREVSMSKVDFF--IJKSYRNQDOSMGEMQIIGGDLSTLAGNFLIV
RA	Db	87	LLDIAVQTYGSSESSVPPFFEVYVRLQYQNDSNTGQTRVL-DDDLISFRDGHVLIV
RA	RA	145	145
RA	Qy	134	EDVUGTGTRTMKALLSMIEKXKPNNMKVASLVLKRTSRSDGFRPDYAGFEIPHLFVYGYAL
RA	Db	146	EDIVDTGFTLTFEGRKLAVGPKMSRATLVEKRTDRNSNLKGDPVGSTSIEDWVVGCCY
RA	RA	193	193
RA	Qy	194	DYNEYFRLNHCIVNNE
RA	Db	206	DFNEMFRDFDHVAVLSD
RA	RA	222	
RA	RESULT	12	
RA	HPRT	BACSU	STANDARD;
RA	ID	HPRT	BACSU
RA	AC	P37472;	PRT;
RA	AC	01-OCT-1994	180 AA.
RA	DT	(Rel. 30, Created)	
RA	DT	01-OCT-1994	
RA	DT	(Rel. 30, Last sequence update)	
RA	DT	28-FEB-2003	
RA	DE	(Rel. 41, Last annotation update)	
RA	DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGRT)	
RA	DE	(HGRTase).	
RA	GN	HGRT	
RA	OS	Bacillus subtilis.	
RA	OC	Firmicutes; Bacillales; Bacillaceae; Bacillus.	
RA	OC	NCBIX-TaxID=1423;	
RA	RN	[1]	
RA	RP	SEQUENCE FROM N.A.	
RA	RC	SEQUENCE FROM N.A.	
RA	RA	P37472;	
RA	RA	01-OCT-1994	
RA	RA	(Rel. 30, Created)	
RA	RA	01-OCT-1994	
RA	RA	(Rel. 30, Last sequence update)	
RA	RA	28-FEB-2003	
RA	RT	(Rel. 41, Last annotation update)	
RA	RT	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGRT)	
RA	RT	(HGRTase).	
RA	DN	[2]	
RA	RN	DNA Res. 1:1-14 (1994).	
RA	RP	SEQUENCE FROM N.A.	
RA	RC	STRAIN=168;	
RA	RX	MEDLINE=91044033; PubMed=938377;	
RA	RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,	
RA	RA	Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchart S.,	
RA	RA	Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,	
RA	RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,	
RA	RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,	
RA	RA	Devitz F., Devitz K.M., Ehrlich S.D., Emmerson P.T.,	
RA	RA	Entian K.D., Ferrington J., Fabre C., Ferrer P., Fouquer D.,	
RA	RA	Strand 109	
RA	RA	113	

Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Hilbert H., Halsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karimata D., Kasahara Y., Klaerr-Bianchi M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kunano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauli C., Medina N., Meliello R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwolik S., Prescott A.M., Presecan E., Puic P., Purnelle B., Rapoport G., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Saco T., Scanian E., Schleicher S., Schroeter R., Scorfione F., Sekiguchi J., Sekowska A., Sevor S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Tachikawa M., Uchiyama S., Vandembol M., Vannier F., Vassarotti A., Tosato V., Uchimatsu A., Tanaka T., Terpstra P., Tognoni A., Vizzi A., Wambier R., Wedderburn E., Weitzenecker T., Winters P., Wipat A., Yamane K., Yamamoto K., Yata K., Yoshida K., Yoshihikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> ," <i>Nature</i> 390:249-256 (1997).	207 VI 208
-!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-alpha-D-ribose 1-diphosphate	QY
-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.	Db
-!- PATHWAY: Purine salvage	
-!- SUBCELLULAR LOCATION: Cyttoplasmic	
-!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY	
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EMBL; D26185; BAA05103.1; -.	
PIR; S29104; CAB11844.1; -.	
HSSP; S660938; S660938.	
RSSP; P51900; 1HGK.	
SubList; BG10131; hprt.	
InterPro; IPR005904; HxN phospho trans.	
InterPro; IPR002375; Pro-DP rp transf.	
InterPro; IPR00036; PRtransferase.	
Pfam; PF00156; Ribosyltran.	
TIGRFAMS; TIGR01203; HGPRTase; 1.	
PROSITE; PS00103; PUR_PUR_PR_TRANSFER; 1.	
Transfere; Glycosyltransferase; Purine salvage; Magnesium; Complete proteome.	
METAL; 99 MAGNESIUM (BY SIMILARITY).	
METAL; 100 100 MAGNESIUM (BY SIMILARITY).	
SEQUENCE 180 AA; 20239 MW; 5D247BB644A57D2 CRC64;	
Query Match 23.8%; Score 265.5%; DB 1; Length 180;	
Best Local Similarity 36.8%; Pred. No. 2.4e-15; Indels 17; Gaps 7;	
Matches 67; Conservative 35; Mismatches 63; Insert 17; Gaps 7;	
31 DLEYVLLPHGIFTVDRIERLAKMDIGYDMSIMVLC--VLKGCGYKFACDLYBHLKNTSRN 88	
5 DIEKVLISSEEQKVKYKELGALTESE--YQDTPPLAIGVKGALPFWADLKH----- 56	
89 SDRFYSMKVDEFLRKLYSYRNQ-SMGEMQIIGGDLST-LAGKNEFLIVEDVGTGRTMKA 146	
57 -DTYLEM--DMDVSYGNSTYSSGEVKKI--KDLDTSVGRDILIDBDGTLTSYL 111	
147 LSNIKVKYKPNMKVAVLILVKRTSRSDGFRDVAGFE-PHLFVYGAQDLYNEYFRDLMHIC 206	
112 VELFPLVYKPKVSKVTKMILNKGSKPDKDIAEVGIVPFDVDAWVQWIDYVTPYDTC 177	
RESULT 13	
HPRT-LACIA STANDARD; PRT; 183 AA.	
ID HPRT-LACIA	
AC 002522;	
DT 01-JUL-1993 (Rel. 26, Created)	
DT 01-JUL-1993 (Rel. 26, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGprt)	
DE (HPRTase).	
HPT OR LL0020.	
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus	
[1] _TAXID=1360;	
SEQUENCE FROM N.A.	
STRAIN=CJCC2285;	
MEDLINE=93101141; PubMed=1465108;	
RA Nilsson D., Lauridsen A.A.;	
OX RN	
RP	
RC	
RN MEDLINE=93101141; PubMed=1465108;	
RA	
RT "Isolation of Purine auxotrophic mutants of <i>Lactococcus lactis</i> and characterization of the gene <i>hpt</i> encoding hypoxanthine guanine phosphoribosyltransferase.";	
RT Mol. Gen. Genet. 235:359-364 (1992).	
RT [2]	
SEQUENCE FROM N.A.	
STRAIN=IL1403;	
RC MEDLINE=21235186; PubMed=11337471;	
RX	
RA Bolotin A., Wincker P., Mauger S., Jaiillon O., Malarme K., Weissenbach J., Bhrlich S.D., Sorokin A.;	
RT "The complete genome sequence of the lactic acid bacterium <i>Lactis</i> ssp. <i>Lactis</i> IL103.";	
RT Genome Res. 11:731-753 (2001)	
RL -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-alpha-D-ribose 1-diphosphate.	
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.	
CC -!- PATHWAY: Purine salvage.	
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.	
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.	
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CC EMBL; X67105; CAA47404.1; -.	
CC EMBL; X69123; CAA48876.1; -.	
CC EMBL; AE006241; AAK04118.1; -.	
CC PIR; D86627; D86627.	
CC PIR; S30100; S30100.	
CC HSSP; P00492; 1HMP.	
CC InterPro; IPR005904; HxN phospho trans.	
CC InterPro; IPR002375; Pro-DP rp transf.	
CC InterPro; IPR00036; PRtransferase.	
CC Pfam; PF00156; Ribosyltran.	
CC TIGRFAMS; TIGR01203; HGPRTase; 1.	
CC PROSITE; PS00103; PUR_PUR_PR_TRANSFER; 1.	
CC Transfere; Glycosyltransferase; Purine salvage; Magnesium; Complete proteome.	
CC METAL; 99 MAGNESIUM (BY SIMILARITY).	
CC METAL; 100 100 MAGNESIUM (BY SIMILARITY).	
CC SEQUENCE 180 AA; 20239 MW; 5D247BB644A57D2 CRC64;	
Query Match 23.8%; Score 265.5%; DB 1; Length 180;	
Best Local Similarity 36.8%; Pred. No. 2.4e-15; Indels 17; Gaps 7;	
Matches 67; Conservative 35; Mismatches 63; Insert 17; Gaps 7;	
31 DLEYVLLPHGIFTVDRIERLAKMDIGYDMSIMVLC--VLKGCGYKFACDLYBHLKNTSRN 88	
5 DIEKVLISSEEQKVKYKELGALTESE--YQDTPPLAIGVKGALPFWADLKH----- 56	
89 SDRFYSMKVDEFLRKLYSYRNQ-SMGEMQIIGGDLST-LAGKNEFLIVEDVGTGRTMKA 146	
57 -DTYLEM--DMDVSYGNSTYSSGEVKKI--KDLDTSVGRDILIDBDGTLTSYL 111	
147 LSNIKVKYKPNMKVAVLILVKRTSRSDGFRDVAGFE-PHLFVYGAQDLYNEYFRDLMHIC 206	
112 VELFPLVYKPKVSKVTKMILNKGSKPDKDIAEVGIVPFDVDAWVQWIDYVTPYDTC 177	

Best Local Similarity	33.7%	Pred.	No. 5.9e-15;
Matches	60;	Conservative	45;
Mismatches	61;	Indels	12;
Gaps	4;		
Qy	32 LEYVILPHGLIVDRLAKIDMIDIGSDIMVLCVKGKYGKFCADLVHKNISRNSDR 91	Matches	62;
Db	10 TEKVLYSEETTIESKELLSKEETLKEYEGNPLVIGLRSVPFLAELKHID----- 61	Conservative	40;
Qy	92 FVSMKVDFIRLKSYSR-NDQSMGEMQIIGGGDLSTLAGKFLNVLVEDVYGTGRTMKALLSNI 150	Mismatches	64;
Db	62 -CHLIEDTMVIVSSTHGTTKSGEVLLD-YTAVKGDLILVEDIITDGTLYKELL 119	Indels	12;
Qy	151 EKYKENMIKVASLLVVKRTSRSDGFRPDIYAGFEIPLHFLFVYGA LDYNEYFRDLNHCIVI 208	Gaps	5;
Db	120 EHGRAN-VKTVTLDDKPGERIVEKPDYSGFTIPNEFVFGFLDYEENYRNLPXVGVL 176		
RESULT 14			
HPRT_AQAE	HPRT_AQAE	STANDARD;	PRT;
ID	HPRT_AQAE		178 AA.
AC	06681;		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.-)		
DE	(HGprtase)		
GN	HPRT		
OS	OS OR AQ		
OS	Aquifex aeolicus.		
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.			
OX	NCBI_TaxID=63363;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=VF5;		
RX	MEDLINE=98196666; PubMed=9537320;		
RA	Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,		
RA	Graham D.E., Overbeek R., Snead M.A., Keiller M., Aujay M., Huber R.,		
RA	Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,		
RT	"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus."		
RL	Nature 392:353-358(1998).		
CC	-I- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5'-phospho-		
CC	alpha-D-ribose 1-diphosphate.		
CC	-I- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5'-phospho-		
CC	alpha-D-ribose 1-diphosphate.		
CC	-I- PATHWAY: Purine salvage.		
CC	-I- SUBCELLULAR LOCATION: Cyttoplasmic.		
CC	-I- SIMILARITY: BELONGS TO THE PURINE/PRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.		
CC			
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: A000695; AAC06788; 1; -.		
DR	PIR: A70349; A70349.		
DR	HSSP: P00422; 1HMP.		
DR	InterPro: IPR00504; Hxn_Pphospho_trans.		
DR	InterPro: IPR005375; Pr_PyP_rp_transf.		
DR	InterPro: IPR00836; PRTransfase.		
DR	PFam: PF00156; Priboxytrian; 1.		
DR	TIGRFans: TIGR01203; HGPrase; 1.		
DR	PROSITE: PS00103; PUR_PYR_PR_TRANSFER; 1.		
KW	Complete proteome.		
FT	METAL 102 102 MAGNESIUM (BY SIMILARITY).		
FT	METAL 103 103 MAGNESIUM (BY SIMILARITY).		
SQ	SEQUENCE 178 AA;	Score 255; DB 1;	Length 178;
Query Match	Best Local Similarity	34.8%;	Pred. No. 1.8e-14;

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 CC or send an email to license@isb-sib.ch).

DR EMBL; L08622; AAC37202.1; -
 DR PDB; 1HGX; 17-AUG-96.
 DR InterPro; IPR00504; HxN_phospho_trans.
 DR InterPro; IPR002375; Pr/PY_PTP_trans.
 DR InterPro; IPR000836; PRtransf erase.
 DR PFam; PF00156; Pribnowtran; 1.
 DR TIGRFAMS; TIGR01203; HGPtrans; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 DR KW Transferase; Glycosyltransferase; purine salvage; Magnesium; 3D-structure.
 KW METAL 102 102 MAGNESIUM.
 FT METAL 103 103 MAGNESIUM.
 FT TURN 8 9 MAGNESIUM.
 FT STRAND 10 15 MAGNESIUM.
 FT HELIX 17 35 MAGNESIUM.
 FT TURN 36 38 MAGNESIUM.
 FT S-STRAND 41 45 MAGNESIUM.
 FT TURN 46 49 MAGNESIUM.
 FT HELIX 50 57 MAGNESIUM.
 FT TURN 58 59 MAGNESIUM.
 FT STRAND 65 72 MAGNESIUM.
 FT STRAND 87 87 MAGNESIUM.
 FT TURN 94 95 MAGNESIUM.
 FT STRAND 97 105 MAGNESIUM.
 FT HELIX 109 119 MAGNESIUM.
 FT TURN 120 121 MAGNESIUM.
 FT STRAND 125 134 MAGNESIUM.
 FT STRAND 147 152 MAGNESIUM.
 FT STRAND 157 159 MAGNESIUM.
 FT TURN 160 161 MAGNESIUM.
 FT STRAND 162 162 MAGNESIUM.
 FT STRAND 164 164 MAGNESIUM.
 FT TURN 165 166 MAGNESIUM.
 FT STRAND 167 167 MAGNESIUM.
 FT TURN 169 170 MAGNESIUM.
 FT STRAND 174 177 MAGNESIUM.
 FT HELIX 179 183 MAGNESIUM.
 SQ 183 AA; 21091 MW; A151B2F5D7D1C214 CRC64;
 Query Match 21.0%; Score 234.5; DB 1; Length 183;
 Best Local Similarity 32.4%; Pred. No. 9; se-13;
 Matches 59; Conservative 37; Mismatches 73; Indels 13; Gaps 4;
 Qy 31 DLEYVILPHGIVYDRIERPLAKDMDIGYSDIMVLCYLRGGYKFCADLVEHLKNISRNSD 90
 Db 9 DLERVLYNQDDQKRTRLELAALTEFVDKPNPVMICVLTGAVPFYDLLKHID----- 61
 Qy 91 RFVSMKVDFIRLKSYRANDQSMGEMQIIGGDLST-LAGKNFLIVEDYVGRTMKALLSN 149
 Db 62 -FQLEPDYIICSSYSGTSTGNLTI--SKDLKTNIEGRHVIVEDIDTGLTMYQULLNN 117
 Qy 150 IEKYKPNMIIKVASLLVYKRTSRSDFPFI-DYIGGFEIPLFLVGGYALDYNEYRDLNHCIV 208
 Db 118 LOMRKPSLKVCTLCDRIGKRAYDVPIDYCGFVVERNYIICYGFDFHNKYRNLPVIGIL 177
 Qy 209 NE 210
 Db 178 KE 179

Search completed: November 13, 2003, 15:05:31
 Job time : 18 secs

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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:02:56 ; Search time 35 Seconds

(without alignments)

1563.061 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: MATRSPGVIMDDWPGYDNL.....LDNEYFRDLNHCIVNEHG 212

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 830525 seqs, 25805604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23 :*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_hexameric:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodococcus:*

12: sp_rhizobacter:*

13: sp_rhizobacteri:*

14: sp_rhizobacteri:*

15: sp_rhizobacteri:*

16: sp_rhizobacteri:*

17: sp_archaeap:*

17 346 31.0 279 5 Q27375 toxoplasma

18 306 27.4 84 6 Q29494 macropus ro

19 294 26.3 85 6 P79306 sus scrofa

20 290.5 26.0 115 11 Q55061 mesocricetus

21 272 24.4 76 6 Q97876 ornithorhynchus

22 270.5 24.2 183 16 Q8XHL2 clostridium

23 265.5 23.8 180 16 Q9CFF99 lactococcus

24 265 23.7 76 6 Q97875 monodelphis

25 265 23.7 76 6 Q97873 macropus eu

26 265 23.7 76 6 Q97872 isodon mac

27 257.5 23.1 178 16 Q97EB1 clostridium

28 257.5 23.1 180 16 Q8P321 streptococcus

29 257 23.0 176 16 Q8K977 chlorobium

30 254.5 22.8 648 16 Q92E56 listeria in

31 252 22.6 76 6 Q97871 isodon mac

32 251.5 22.5 181 16 Q8R7L0 thermoanaerobacter

33 251.5 22.5 194 16 Q8NM82

34 250.5 22.4 648 2 Q8KU03

35 250.5 22.4 648 16 Q8YAC7

36 247.5 22.2 180 16 Q97C4 streptococcus

37 247.5 22.2 180 16 Q8DRP8

38 246.5 22.1 184 16 Q8EUI7

39 246 22.0 175 16 Q8RGK5

40 245 22.0 76 6 Q97874

41 244.5 21.9 175 2 Q9ZNK6

42 242.5 21.7 238 5 Q95ZC9 leishmania

43 241 21.6 212 16 Q8FMG1 corynebacterium

44 239.5 21.5 179 16 Q99W93

45 239 21.4 241 5 Q9U6Y2 leishmania

ALIGNMENTS

RESULT 1

Q9NRG1 PRELIMINARY; PRT; 225 AA.

AC Q9NRG1; ID Q9NRG1; DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DB HHGP (HHGP protein).

GN

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthidae; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN [1] NCBI_TaxID:9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Liver cancer;

RA Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.; "A novel gene expressed in human liver cancer tissue.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Koma I., Hara R., Takeuchi K., Arita M., Nabebara T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Negishi K., Masuho Y., Oshima A.;

RT "NEDO human cDNA sequencing Project.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF226056; AAF86956; 1.;

DR EMBL; AR021950; BAB13944; 1.;

DR EMBL; BC008662; AAH08662; 1.;

DR HSSP P00492; 1HMP.

DR InterPro; IPR005904; Hxn_phospho_trans.

SUMMARIES

Result No. Score Match Length DB ID Description

1 1065 95.4 225 4 Q9NRG1 Q9nr91 homo sapiens

2 786 70.4 218 11 Q60466 Q60466 cricetus

3 782 70.1 218 11 Q99KF5 Q99KF5 mus musculus

4 779 69.8 218 11 Q64401 Q64401 cricerulus

5 746 66.8 210 11 Q9JK76 Q9jk76 akodon curs

6 658 59.0 186 6 Q9GJT9 Q9gjt9 bos taurus

7 553 49.6 161 11 Q9JK75 Q9jk75 akodon curs

8 543 48.7 154 6 Q46381 Q46381 orctolagus

9 470 42.1 142 6 Q9XSI4 Q9xsi4 sus scrofa

10 456 40.9 135 6 Q28968 Q28968 sus scrofa

11 455 40.8 193 6 Q28530 Q28530 macropus ro

12 446 40.0 231 5 Q96085 Q96085 plasmodium

13 445.5 39.9 231 5 Q8LJS1 Q8ljs1 plasmodium

14 437 39.2 136 6 Q52558 Q95258 sus scrofa

15 430.5 38.6 214 5 Q9nf11 Q9nf11 caenorhabditis

16 400 35.8 203 5 Q03925 Q03925 plasmodium

DR	PROSITE; PS00103; PUR PYR PR TRANSFER;	1.	Qy	129 NFLIVEDVGTGRTMALLSNIKEKPNTKVASLILVKRTS	169
KW	Glycosyltransferase; Transferase.		Db	121 NVLIVEDDTGKTMQTLSSVKQNPQVKVASLILVKRTS	161
FT	NON TER 1				
FT	NON TER 186	186			
SEQUENCE	186 AA; 20933 MW; 546486338FC42865	CRC64;			
SQ					
Query Match	59 0% ; Score 658; DB 6; Length 186;		RESULT 8		
Best Local Similarity	65.1% ; Pred. No. 1.3e-50;		ID	046381 PRELIMINARY;	PRT; 154 AA.
Matches 122; Conservative 32; Mismatches -33; Indels 0; Gaps 0;			AC	046381;	
Best Local Similarity	65.1% ; Pred. No. 1.3e-50;		DT	01-JUN-1998 (TREMBREL. 06, Created)	
Matches 122; Conservative 32; Mismatches -33; Indels 0; Gaps 0;			DT	01-JUN-1998 (TREMBREL. 06, Last sequence update)	
Qy	15 PGYDLNLFTYQPHYQGDLLEYVLIIPHGLIVDRIERLAKDMDIGYSDIMVLCVULKGGYKF 74		DT	01-MAR-2003 (TREMBREL. 23, Last annotation update)	
Db	1 PGYDLNLFC1PNH2TAEDLLEYVFIPIGLIMRTLARDYKEMGGHHTVALCALKGGYKF 60		DE	Hypoxanthine phosphoribosyltransferase (Fragment).	
Qy	75 CADLYEHLKNISRNDRFVNKVDIFRLKSYRNDGSMGENQIIGGDLSTLAGRNFLIVE 134		OS	Oryctolagus cuniculus (Rabbit).	
Db	61 FADLLDYKZLNRSNDSK50MTVDIFRLKSYCNDGTDGKVIGGDDLSLTGKVNVLIVE 120		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
Qy	135 DVVGTGRTMALLSNTIEKYPNMIKVASLILVKRTTSRSDGPRDYAGFEIPLHLYVGYALD 194		NCBI_TaxID	99865;	
Db	121 DIDIQKTMQTLALLVYKHPKPVKVASLIMKRTPKPSVGKPDFVGFELDKFVGYALD 180		OX		
Qy	195 YNEYPR 200		RN		
Db	181 YNEYSR 186		RP	SEQUENCE FROM N.A.	
SEQUENCE FROM N.A.			RC	STRAIN=New Zealand White;	
RA	Boyle R. H.; Sciore P.; Reno C.; Marchuk L.; Frank C. B.; Hart D. A.;		RA	"Cloning, sequencing, and expression of extracellular matrix molecules in normal and healing rabbit ligament by RT-PCR. ;	
RT	RT in normal and healing rabbit ligament by RT-PCR. ;		RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.	
CC	-; SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.		CC	-	
EMBL	AF00294; AAC8878864; 1;		CC		
DR	HSSP; P00492; 1HMP.		DR		
DR	InterPro; IPR005904; HxtN phosphotrans.		DR		
DR	InterPro; IPR002375; PR_PYR_P transferase.		DR		
DR	InterPro; IPR000836; PR_PYR_P transferase.		DR		
PFam	PF001156; Pribosyltran; 1.		DR		
TIGRFAMS	TIGR01203; HGPRTase; 1.		DR		
DE	PROSITE; PS00103; PUR PYR PR TRANSFER; 1.		DR		
GN	Glycosyltransferase; Transferase.		FT		
GN	NON TER 1.		FT		
OS			FT		
OC	154 AA; 17326 MW; FDBD6F796DF07B2A CRC64;		FT		
OC	SEQUENCE		FT		
NCBI_TaxID	29096;		FT		
RN			FT		
RP	SEQUENCE FROM N.A.		FT		
RA	Bonvicino C.R.B.; Moreira M.A.M.; Arcuri R.A.; Seuanez H.N.;		FT		
RT	"Induction and Characterization of Hypoxanthine Phosphoribosyltransferase (hprt) Deficient Cell Lines of Akodon cursor." (TREMBREL. 15, Last sequence update)		FT		
RT	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		FT		
RL	-; SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.		FT		
CC	EMBL; AF054384; AAC70287.1; -.		FT		
DR	HSSP; P00492; 1BZY.		FT		
DR	InterPro; IPR005904; HxtN phosphotrans.		FT		
DR	InterPro; IPR002375; PR_PYR_P transferase.		FT		
DR	InterPro; IPR000836; PR_PYR_P transferase.		FT		
DR	PFam; PF001156; Pribosyltran; 1.		FT		
DR	TIGR01203; HGPRTase; 1.		FT		
DR	PROSITE; PS00103; PUR PYR PR TRANSFER; 1.		FT		
KW	Glycosyltransferase; Transferase.		FT		
FT	NON TER 1.		FT		
SEQUENCE	161 AA; 18153 MW; FE8305EAF248EF17 CRC64;		FT		
SQ			FT		
Query Match	49 6% ; Score 553; DB 11; Length 161;		RESULT 9		
Best Local Similarity	64.6% ; Pred. No. 2.3e-41;		ID	09X514 PRELIMINARY;	PRT; 142 AA.
Matches 104; Conservative 27; Mismatches 30; Indels 0; Gaps 0;			AC	09X514;	
Qy	9 VIMDDWPGYDINLFTYQPHYQGDLLEYVLIIPHGLIVDRIERLAKDMDIGYSDIMVLCVU 68		DT	01-NOV-1999 (TREMBREL. 12, Created)	
Db	1 VISDDEPGYDIDLFC1PNH2TAEDLLEYVFIPIGLIMRTLARDYKEMGGHHTVALCALKG 60		DT	01-NOV-1999 (TREMBREL. 12, Last sequence update)	
Qy	69 KGGYKFCADLYEHLKNISRNDRFVSMKTVDFIRLKSYRNDSMGENQIIGGDLSTLAGK 128		DE	Hypoxanthine phosphoribosyltransferase (Fragment).	
Db	61 KGGYKFFTDLDYKALNRSNDRS1PMTVDFIRLKSYCNQDSTGDFKVGDDLSLTGK 120		OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
RN			NCBI_TaxID	9823;	
RP	SEQUENCE FROM N.A.		RC	STRAIN=Andraise x Large White;	
RA			RA	Steinborn R., Balasch M., Plana-Duran J., Klein D., Goeroffy A.,	

DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	RA	Fraser C.M., Barrell B.
GN	HGPRT.	RT	"Genome sequence of the human malaria parasite Plasmodium falciparum."
OS	Plasmodium berghei	RL	Nature 419:498-511(2002).
OC	Plasmodium; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	DR	EMBL; AE014830; AAN35319..1; -.
OX		KW	Transferase; Glycosyltransferase..
RN	[1]	SQ	SEQUENCE 231 AA; 263625 MW; BCD3B30486DD287 CRC64;
RP	SEQUENCE FROM N.A.	Query Match	39.9%; Score 445.5; DB 5; Length 231;
RC	STRAIN=XAT;	Best Local Similarity	42.7%; Pred. No. 1.3e-31;
RX	MEDLINE=1165804; PubMed=1129277; RA	Matches	93; Mismatches 74; Indels 11; Gaps 3;
RT	Onida T., Miyamoto K., Sugioka Y., Kangawa K., Kano S., Suzuki M.;	QY	5 SPGV-----VIMDWPGYDNLNFTYPQHGGDLEYVPLPHGTIVDRIBERLAKDMDI 57
RT	"Suppressed expression of hypoxanthine-guanine phosphoribosyltransferase (HGPRT) in an irradiation-attenuated	Db	6 NPGAGNAFDPFVFKDDGYDLDSEMPAHYKYLTKVLPGNGVINKRERKLAYDKKVV 65
RT	Plasmodium berghei XAT strain."	QY	58 GYSDIMVLCVKGYYKFCADLVEHLKNISRNSDRFVSMKV--DFIRLKSYRNDOSGMGEM 114
RL	Parasitol. Int. 48:157-167(1999).	Db	66 NNEEFPHILCLLKGSRGFFTALLKLHSRHINNSAVETSKPLFGEHYVRVKSYCNDQSTGTL 125
CC	-1- SIMILARITY: BELONGS TO THE PURINE-BYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.	QY	115 QIIGGGDLSTLAGKFLIVEDVVGTRTMKALLSNIEKYPNMIKVASLUVKRTSRSDGF 174
DR	EMBL; AB020412; BA34691.1; -.	Db	126 BIV-SEDLSSCLKGHLVHLVPLKFCBVKKPEKJITVIAACLFIKRTPLWNGP 184
DR	HSSP; P20035; 1CJB.	QY	175 RPDYAGGEIPLHFVYGAQYALDNEYFRDLNHCIVNEHG 212
DR	InterPro; IPR005904; Hxn phospho transf.	Db	185 KADFVGSFISIDPHFVYGSLDYNEIFRDLDHICLVLNDEG 222
DR	InterPro; IPR002375; Pr/Py-TP_t-transf.	QY	RESULT 14
DR	PFam; PF00156; Priboosyltran. 1.	ID	Q95258
DR	TIGRFAMS; TIGB01203; HGprtase; 1.	AC	Q9558; PRELIMINARY;
DR	PROSITE; PS00103; EUR_PPR_PR_TRANSFER; 1.	DT	DT 01-FEB-1997 (TREMBLrel. 02, Created)
DR	KW Glycosyltransferase; Transferase.	DB	DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
SEQUENCE	231 AA; 263625 MW; C02BFE45CDB8B72 CRC64;	DB	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update).
RP	Query Match	40.0%; Score 446.5; DB 5; Length 231;	
RC	Best Local Similarity	42.7%; Pred. No. 1.1e-31;	
RX	Matches 91; Conservative 41; Mismatches 66; Indels 15; Gaps 4;	QY	68 LKGYYKFCADLVEHLKNI-----SRNSDRFVSMKVDFIRLKSYRNDOSGMGEMQITG 119
RT	VIMWDWPGYDNLNFTYPQHGGDLEYVPLPHGTIVDRIBERLAKDMDI 67	Db	76 LKGSRSFTSLLKYLDRHNNYYADASTNSYR----EHYVRVKSYCNTGCTGRLEIV-S 129
RT	VMKDD-DG-EFDSEVTPDHYKNYLKRILPNGLKSRSRMAFDISRYNGEKFHLCL 75	QY	120 GDLSLAGKFLIVEDVVGTRTMKALLSNIEKYPNMIKVASLUVKRTSRSDGRPDYA 179
RT	InterPro; IPR002375; Pr/Py-TP_t-transf.	Db	130 EDLSSCLKGKVLIVEDIDGNTLSKEDYKPLFPTKAVASALYIKRTPLWNGPKADFT 189
RT	InterPro; IPR00836; Pstransferase.	QY	180 GFEIPHLFVYGAQYALDNEYFRDLNHCIVNEHG 212
RT	PFam; PF00156; Priboosyltran. 1.	Db	190 GFSVENFFFLVCGLDYNEFRDLNEVCIISSEG 222
RP	SEQUENCE FROM N.A.	QY	RESULT 13
RC	Q8JJS1 PRELIMINARY;	ID	Q8JJS1
AC	Q8JJS1; PROSITE; PS00103; EUR_PPR_PR_TRANSFER; 1.	AC	Q8JJS1
DT	01-MAR-2003 (TREMBLrel. 23, Created)	DR	InterPro; IPR002375; Pr/Py-TP_t-transf.
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DR	InterPro; IPR00836; Pstransferase.
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR	PFam; PF00156; Priboosyltran. 1.
GN	PF10_0121.	DR	PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
OS	Plasmodium falciparum (isolate 3D7).	DR	Glycosyltransferase; Transferase.
OC	Plasmodium; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	FT	FT NON_TER 1
RN	[1]	FT	FT NON_TER 1
RP	SEQUENCE FROM N.A.	FT	FT NON_TER 1
RC	STRAIN=3D7;	FT	FT NON_TER 1
RX	MEDLINE=22255705; PubMed=12368864;	FT	FT NON_TER 1
RA	Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,	FT	FT NON_TER 1
RA	Cartron J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,	FT	FT NON_TER 1
RA	Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,	FT	FT NON_TER 1
RA	Chan M.-S., Nene V., Shallom S.J., Suh H., Peterson J., Angioli S.,	FT	FT NON_TER 1
RA	Pereira M., Alien J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,	FT	FT NON_TER 1
RA	Martin D.M.A., Fairlamb A.H., Fraunhofer M.J., Roos D.S., Ralph S.A.,	FT	FT NON_TER 1
RA	McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Hoffman S.L., Newbold C., Davis R.W.,	FT	FT NON_TER 1
RA	Venter J.C., Carucci D.J., Hoffman S.L., Hoffman S.L., Newbold C., Davis R.W.,	FT	FT NON_TER 1
RP	Query Match	39.2%; Score 437; DB 6; Length 136;	
RC	Best Local Similarity	63.1%; Pred. No. 3.7e-31;	
RX	Matches 82; Conservative 26; Mismatches 22; Indels 0; Gaps 0;	QY	47 ERLARDIMKDIGYSDIMWVLCVLRGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSYR 106
RA	1 ERLARDVVKEMGGHHIVALCVLKGYYKFADLDDYTKALRNRSNSDIPMTVDFFRLKSYC 60	Db	107 NDQSMGEMOIIGGDLSTLAGKFLIVEDVVGTRTMKALLSNIEKYPNMIKVASLUVK 166
RA	61 NDQRTGDIKVIGGDDSLTGTGNVLIVEDIDGKTMQITLLSLVQHNPFRMVKVASLUVK 120	Db	167 RTSSRSDGFRP 176

RESULT 15						
Db	121	RTPRSVYRPF	130			
Q9NF11		PRELIMINARY;				
ID	Q9NF11					
AC	Q9NF11;					
DT	01-OCT-2000	(TREMBLrel. 15, Created)				
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)				
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)				
DE	Y10588B.5	protein.				
DE	Y10588B.5	protein.				
GN	Caenorhabditis elegans.					
OS	Caenorhabditis elegans.					
RA	Sulston J E.					
RL	Submitted (SEP-2001)	to the EMBL/GenBank/DDBJ databases.				
[1]						
RN		SEQUENCE FROM N.A.				
RP		MEDLINE=90069613; PubMed=9851916;				
RX		none;				
RA		"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology."				
RT		Science 222:2012-2018(1998).				
RL		EMBL: AL122877; CAB0853.1; -.				
DR		HSSP: P00492; 1HMP.				
DR		WormBase: Y10588B.5; CE24099.				
DR		InterPro: IPR005904; Hxn phospho trans.				
DR		InterPro: IPR000836; PRTRTransferase.				
PFam		PF00156; Pribosyltran; 1.				
DR		TIGRFAMS; TIGR01203; HGPRTase; 1.				
KW		Transferase.				
SQ		SEQUENCE 214 AA; 23824 MW; 55FABB1241B039D CRC64;				
Qy		Query Match	38.6%	Score 430.5;	DB 5;	Length 214;
Best Local Similarity	46.6%	Pred. No. 2.5e-30;				
Matches 95;	Conservative	Mismatches 28;	Indels 78;	3;	Gaps	
Db		9 VIMMDPQGYDNLFTYQPHYQDLEYVLIPIGIIIVDIERAKDMDIGSDIMVLCVL				
7 VIPDDFE-LPVDADFPICYDQDLSGVVIEPLSVRVRVRLAKDTHAEIGNKPIALCVL						
Qy		69 KGGYKEFADLVEHKLNTSRNSDRFVSNKVDIFRLKSYRNDMSGMENQIGGGDLSTLAKK				
Db		66 KGSYKPTALVELTNAARSSCP - PMTVDFTRVSKYEDQNOSTGQIQMGLSNDELKGK				
Qy		129 NFLIVEDVVGTRTMKALLSNIEKYKPNMIKVASLIVKRTSRSDGFRPDYAGEFIPHLFV				
Db		124 SVLVVDDISDGTTLAKLSTLHETGVKTNTLLSKRVKRVDVDPFDYFAEIPDKF1				
Qy		189 VGYALDNEYFEDLNLHICVINHBG 212				
Db		184 VGYGDYDYNOKRFDLGHICUMSPAG 207				

Search completed: November 13, 2003, 15:06:19
Search time: 36 sec

Gencore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 4, 2003, 12:13:13 ; Search time 2584 Seconds
 (without alignments)

3356.363 Million cell updates/sec

Title: US-09-902-705-2
 Perfect score: 1116
 Sequence: 1 MATRSPGVIMDDPGYDIN.....LDNEYFRDLNHCVINEHG 212

Scoring table: BLOSUM62
 Xgapext 10.0 , Xgapext 0.5
 Ygapext 10.0 , Ygapext 0.5
 Fgapext 6.0 , Fgapext 7.0
 Delext 6.0 , Delext 7.0

Searched: 288711 seqs, 20454813386 residues
 Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
 -NODES=_frame+_p2n.model -DEV=slp

Q= /cgn2_1/USPTO_spool_p/US0902705/runat_03102003_085505_27968/app_query.fasta_1
 .391
 -DB=GenEmbl -QFMT=fastap -SUFFIX=std.rge -MINMATCH=0.1 -LOOPCFL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blossum2 -TRANS=human40 cdi -LIST=15
 -OUTPMT=dlo -NORM=next -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US0902705 @runat_03102003_085505_27968 -NCPU=6 -ICPU=3
 -NO_MWA_P -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
 -RGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

Database :
 GenEmbl:
 1: gb_ba: *
 2: gb_htg: *
 3: gb_in: *
 4: gb_m: *
 5: gb_o: *
 6: gb_p: *
 7: gb_ph: *
 8: gb_p1: *
 9: gb_pr: *
 10: gb_ro: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Score	Length	DB ID	Description
1	1.069	95.8	1927	6	AR310478 AR310478 Sequence
2	1.065	95.4	807	9	BC026056 Homo sapi
3	1.065	95.4	1450	9	BC008662 Homo sapi
4	1.065	95.4	1926	6	BD159230 Primer fo AR021950 Homo sapi
5	1.065	95.4	1926	9	BD146172 Primer fo X59652 C. longicaud
6	1.038	93.0	783	6	M20011 Mus spretus
7	7.86	70.4	657	10	BC004686 Mus muscu
8	7.83	70.2	702	10	S43335 hprt-hypoxa
9	7.82	70.1	1281	10	X17656 C. longicaud
10	7.79	69.8	685	9	BC000578 Homo sapi
11	7.79	69.8	1222	10	BC000578 Homo sapi
12	7.79	69.8	1316	9	Y00530 Human mRNA
13	7.79	69.8	1331	9	M31642 Human hypox
14	7.79	69.8	1331	9	J00060 Chinese ham
15	7.76	69.5	1301	10	L37778 Meriones un
16	7.76	69.5	1303	10	CRDHPRT

Percent Similarity:	99.51%	Conservative:	2
Best Local Similarity:	98.54%	Mismatches:	1
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US-09-902-705-2 (1-212) x AR310478 (1-1927)			
L29382 Human hypox			
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AR016505 Sequence			
AR096888 Sequence			
BD136083 Vaccines			
J00423 Mouse hypox			
AR215116 Sequence			
AR30358 Sequence			
AR215123 Sequence			
AR30365 Sequence			
M63863 Rat hypoxan			
S79392 hprt=hypoxa			
X62085 R.norvegicus			
BC046003 <i>Danio rer</i>			
AJ13697 <i>Gallus ga</i>			
AF254383 <i>Akodon cu</i>			
AF254384 <i>Akodon cu</i>			
L31700 <i>Macropus ro</i>			
BC047173 <i>Danio rer</i>			
AX071321 Sequence			
AF176419 <i>Bos tauru</i>			
AL831742 <i>Mus muscu</i>			
AF090455 Cloning v			
BD094704 A transge			
Continuation (3 of			
AC127759 <i>Rattus no</i>			
AC096152 <i>Rattus no</i>			
AX526038 Sequence			
M86443 Rat hypoxan			
ALIGNMENTS			
RESULT 1			
AR310478	AR310478	1927 bp	DNA
LOCUS	Sequence 19 from patent US 6558935.		
DEFINITION			
ACCESSION	AR310478		
VERSION	AR310478.1		
KEYWORDS	GT:31703441		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 1927)		
AUTHORS	Tang, Y.T., Corley, N.C., Guegler, K.J., Baughn, M.R., Ial, P., Yue, H., Hillman, J.L. and Azimzai, Y.		
TITLE	Human transferase proteins		
JOURNAL	Patent: US 6558935-A 19 06-MAY-2003;		
FEATURES	Location/Qualifiers		
	1. 1927		
	/organism="unknown"		
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Alignment Scores:			
Pred. No. :	1.11e-106	Length:	1927
Score:	1069.00	Matches:	203
RESULT 2			
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LOCUS	AF226056		
DEFINITION	Homo sapiens HRGP (HHGP)	807 bp	mRNA
ACCESSION	AF226056	mRNA, complete cds.	
VERSION	AF226056.1	GI:9295350	
PRI 20-JUL-2000			

FL1 CDNA									
KEYWORDS		FL1 CDNA							
ORGANISM	Homo sapiens	(human)							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 807)	A novel gene expressed in human liver cancer tissue							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.								
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China								
REFERENCE	2 (bases 1 to 807)	Location/Qualifiers							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	1..807							
TITLE	Direct Submission	/organism="Homo sapiens"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/mol_type="mRNA"							
REFERENCE	3 (bases 1 to 807)	/db_xref="taxon:9606"							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/feature_type="liver cancer tissue"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	1..807							
REFERENCE	4 (bases 1 to 807)	/gene="HHGP"							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	18..695							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/gene="HHGP"							
REFERENCE	5 (bases 1 to 807)	/codon_start=1							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/product="HHGP"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/protein_id="AAF86956..1"							
REFERENCE	6 (bases 1 to 807)	/db_xref="GI:329351"							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/translation="MASSSEA PDYCGWVINDMDPGYDNLVFLTYFOHYXGDIEXVILI PHGIVDRIERKLADIMKDGDSDIMVLCVKGKFCADLVEHLMNSDRFVSM KVDGFLKSYSTRNDOSGMQMOLIGGDDLSLACKNVLIVLVEDVWTGTMTKALLNIEKY KPNMKVAVSLVVRKTSRSDGRFDYXAFEPINLFLVYQYALDYNEXFRDHNHCYNEH GKEXRY"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	239..a							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/origin=							
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REFERENCE	8 (bases 1 to 807)	/length=106..00							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=99.03%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=98.54%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
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REFERENCE	10 (bases 1 to 807)	/score=99.03%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=98.54%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
REFERENCE	11 (bases 1 to 807)	/query_match=9							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	12 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
REFERENCE	13 (bases 1 to 807)	/query_match=9							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	14 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
REFERENCE	15 (bases 1 to 807)	/query_match=9							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	16 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
REFERENCE	17 (bases 1 to 807)	/query_match=9							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	18 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	20 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	22 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	24 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	26 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	28 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
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AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807"							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/length=9							
REFERENCE	30 (bases 1 to 807)	/score=95.43%							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/percentage_similarity=95.43%							
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	/best_local_similarity=95.43%							
REFERENCE	31 (bases 1 to 807)	/query_match=9							
AUTHORS	Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.	/db_xref="taxon:9606..1..807							

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cDNA/>
 Contact: villalon@bcm.tmc.edu.
 Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muñiz, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL site: <http://Image.Lnl.gov>
 Series: IRAK Plate: 13 Row: k Column: 20
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10433254.

Location/Qualifiers

1. .1450
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="Taxon:9606"
 /clone="MGC:16888 IMAGE:3871911"
 /tissue_type="Eye, retinoblastoma"
 /clone_lib="NTB MGC_67"
 /lab_host="DHL0B"
 /note="Vector: PCMV-SPORT6"
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 /translation="WAGSSSEADPDYGRGVIMDDWPGTDLNLLTYPOHYGDLLEVLLPHGIVDPIERLAKDMDIGYSDIMVLCVYKFCADLVHILKNSNSDFVSKKUDFRIASSEYNDOMGEMQIIGGDDLSLACKNVLIVNVETGRTMKALLSIEKVKPNMILKAVSLVLRKTSRSRSGFREDYDAGEFLPFLVVGAYDNEYFDLNHCVINHEK
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BASE COUNT
 ORIGIN

435 a 274 c 318 g 423 t

Alignment Scores:
 Pred. No.: 2.05e-106 Length: 1450
 Score: 1065.00 Matches: 203
 Percent Similarity: 99.03% Conservative: 1
 Best Local Similarity: 98.54% Mismatches: 2
 Query Match: 92.43% Indels: 0
 DB: 9 Gaps: 0

US-09-902-705-2 (1-212) x BC008662 (1-1450)

Qy 7 GlyvalvalleMetaspasptpproGlytyraspLeuAsnLeuPheThrTyProGln 26
 Db 83 GCGCTGAGATATGGATGATGGATGCGGGTACTGTTACTGTTACTACCTACCAAG 142

Qy 27 HisDTrTyGlyAspIeuGluIvrValLeuIleProHisGlyIleLeuAspArgIle 46
 Db 143 CRCTATTGAGACTGGAGATGCTCATGTCATGTTGACGAAATT 202

Qy 47 GluArgLeuAlaLysAspIleMetLysAspIleGlyIleTyrSerAspIleMetValLeuCys 66
 Db 203 GAGCGCTGCCAGATACTTAAAGCATATGATCTGAGACACCTTAAGACATGATCTGCT 262

Qy 67 ValLeuIysGlyIleGlyTyrLyspheCysAlaAspLeuValGluHisLeuLysAsnIleSer 86
 Db 263 GRCCTTAAGAGAGTCAAAATCTGCTGATCTCGAGACACCTTAAGACATCAGC 322

Qy 87 ArgAsnSerAspArgPheValSerMetLysValAspSphIleArgLeuIysSerTyrArg 106
 Db 323 CGAATTCAGATCCATTTGCTCAATAAGGGTGTATCATGACTAAAGTTACAG 382

Qy 107 AspAsnSerAspArgPheValSerMetLysValAspSphIleArgLeuIysSerTyrArg 126
 Db 383 AATGATCCATGCCATGCTGAGATCATAATGCTCAAGCTTCAACGTCGGCT 442

Qy 127 GlyLysAsnSphIleLeuIleValGluAspIleGlyIleGlyAspIleSerIleValLeu 146
 Db 443 GGAAAGATGTTCTATGTTGAGATTTGAGATTTGCTGAGAACTCTGAAAGGACTA 502

Qy 147 LeuSerAsnSphIleLeuIleValGluAspIleValAspIleLeuIleValLeu 166
 Db 503 CTCAAGCTATAGAGAAATACAGGCCAACATGATTAACTGAGCTGAGTGTGGAAAG 562

Qy 167 ArgThrSerArgSerAspGlyIleArgProlAspItyAlaGlyIlePheIleProHisIle 186
 Db 563 AGCACACCCGAGAGTGGGGTTAGAGCTGACTATGTCGATTGATTCAGATCCAACCTTA 622

Qy 187 PheValValGlyTyraIleLeuAspIleAsnGluTyroPheArgAspIleAsnHisIleCys 206
 Db 623 TTCTGGCTGCTATAGGCCCTAGATCATGAACTCATGAACTCATGATCCTGATCCTATGCG 682

Qy 207 ValIleAsnGluHisGly 212
 Db 683 GTCATCATGAGCAGCT 700

RESULT 4
 BD159230

LOCUS BD159230 1926 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD159230

VERSION BD159230.1 GI:27864988

KEYWORDS JP 2002191363-A/14075.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Butleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1226)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,T., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 14073 09-JUL-2002;

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/14073

PD 09-JUL-2002

PF	28-TUL-2000	JP 20000260990	QY	147 LeuSerAsnIleGluLysTyrLysProAsnMetIleLysValAlaSerIeuLeuValLys 166
PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SATO,		Db	489 CTCAGGATATAGAACATAGCCAACTGATTAGCTGAGTCAGTGTGTCGAG 548
PI	JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI		QY	167 ArgThrSerArgSerAspGlyPheArgProLysTyrAlaGlyPheGluLleProHisLeu 186
PC	PC12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, C12P21/02, C12P21/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC		Db	549 AGACATCCGAACTGACGCTTGAACATGCTGATTGACTATGCTGATTGAGTTCCAACCTA 608
	Primer for synthesizing full-length cDNA and use thereof: FH		QY	187 PheValValGlyIleAlaLeuAspTyrAspGluTyrPheArgAspLeuIshisIleCys 206
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	1. .1926	Location/Qualifiers	QY	207 ValIleAsnGluIleGly 212
Source	/organism="Homo sapiens"		Db	669 GTCATGATGAGGACGCT 656
BASE COUNT	590 a	354 c 396 g 586 t	RESULT 5	
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Alignment Scores:			AK021950	AK021950 1926 bp mRNA linear PRI 01-AUG-2002
Pred. No.:	3.03e-106	Length: 1926	LOCUS	AK021950 clone HEMBA1007243, weakly similar to Chinese hamster hprt mRNA.
Score:	1065.00	Matches: 203	DEFINITION	
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Best Local Similarity:	98.54%	Mismatches: 2	VERSION	GI:1043254
Query Match:	95.43%	Indels: 0	KEYWORDS	oligo capping; fis (full insert sequence).
DB:	6	Gaps: 0	SOURCE	Homo sapiens (human)
			ORGANISM	Homo sapiens
			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Butheria; primates; Catarrhini; Hominidae; Homo.
			AUTHORS	1. Isogai,T., Ora,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togia,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshita,A.
			TITLE	NEDO human cDNA sequencing project
			JOURNAL	Unpublished
			REFERENCE	2 (bases 1 to 1926)
			AUTHORS	Isogai,T. and Otsuki,T.
			TITLE	Direct Submission
			JOURNAL	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail: genomics@shri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
QY	7 GlyValIleAlaMetAspAspTyrProGlyTyrAspLeuAsnLeuPheThrTyrProGln 26		COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
Db	69 GGCAGCCTGATATGGATGATGGCAGGTATGACTGAAATTATCAGTACGCCACAG 128		FEATURES	Location/Qualifiers
QY	27 HistYtrTyrGlyAspLeuIleGlyTyrValIleLeuProHisGlyIleIleLeuAspArgIle 46		Source	1..1926
Db	129 CACATATGGAGCTGAGATGAGATGAGATGCTCATCCCTCAGGTATCATTGGAGGATT 188			/organism="Homo sapiens"
QY	47 GluArgLeuAlaLysAspIleIleGlyTyrSerAspIleMetValIleCys 66			/mol_type="mRNA"
Db	189 GAGCCGCGGCCAGGATATTGAAAGCATAGGATATGAGCATCATGCTCTCTGT 248			/db_xref="CAXON:9606"
QY	67 ValIleIysGlyGlyTyrIleGlyTyrAspLeuIalGluIleIysAsnIleSer 86			/clone="HEMBA1007243"
Db	249 GTGCTAAAGGGTTACAAATCTGTGTGTCATGCTGACCTTAAGAATCTGCG 308			/tissue_type="whole embryo, mainly head"
QY	87 ArgAsnSerAspArgPheValSerMetLysValAspPheIleArgLeuLysSerTyrArg 106			
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QY	107 AsnAspGlnSerMetGlyGluMetGlnIleIleGlyIleGlyAspLeuSerThrIleAla 126			
Db	369 AATGCCCCAGTCATGGCTGAGTGGACCCGATGATCTTCACCTGCT 428			
QY	127 GLyIysAsnPheLeuIleValGluAspIleValGlyIleGlyArgThrMetIleAla 146			
Db	429 GAAAGAAATGTTCTCATGTTGAGGTTGAGGTTGAGGAACTGGAGGACCATTAANGCATA 488			

Percent Similarity:	98.54%	Conservative:	1
Best Local Similarity:	98.05%	Mismatches:	2
Query Match:	93.01%	Indels:	1
DB:	6	Gaps:	0
US-09-902-705-2 (1-212) x BD146172 (1-783)			
Qy	7 Glyval1valleMetAspAspThrProGlyTyrAspLeuAsnLeuPheThrTyrProGln 26		
Db	69 GCGCTCTGATTGATGATGATGATGGCAAGGTGACTGAATTATACGTAACCAACAG 128		
Qy	27 HistYtyGlyAspLeuGlyTyrAlaLeuIleLeuValAspArgIle 46		
Db	129 CACTATGGAGCTGGAGTGTGGAGTGTCTCCATGCTATGGAGCAGGATT 188		
Qy	47 GluArgLeuAlaAspIleMetLeuAspIleGlyTyrSerAspIleMetValLeuCys 66		
Db	189 GAGCGCTGCTGCAGGATTAATGAAAGCATAGATGATGATGCTCTGTT 248		
Qy	67 ValLeuLysGlyTyrLysPheCysAlaAspLeuValGluLysAsnIleSer 86		
Db	249 GNCCTAAACGGCTTACATTCGCTGATCTGATCTGATCTGATGAAACACCTTAAGAACATCAGC 308		
Qy	87 ArgAsnSerIspArgPhaValIserIleTyrLeuAspSerTyrArg 106		
Db	309 CGAAATTCAGATCGATTGTCATGAGGTGATTCTCATGACTTAAAGTACAGG 368		
Qy	107 AsnAspGlnSerMetGlyGluGlyIleGlyGlyGlyAspIleSerThrLeuAla 126		
Db	369 AATGACCAAGTCATGGTGAATGAGATGAGATTCACCTTTAACCGTGGCT 428		
Qy	127 GlyLysAsnPheLeuIleLeuValGlyIleGlyArgThrMetLysAlaLeu 146		
Db	429 GCAAGATGTCATGTCAGTGGAGATGTTGCGGAACCTGGAGCCTGAAAGCCTA 488		
Qy	147 LeuSerAsnIleGlyIleIleTyrProLysMetTleIleValLeuValIys 166		
Db	489 CTCAGCATATAGAGATAACAGGCCACATGATTAAGTGTAGTCGTTGTTAAG 548		
Qy	167 ArgThrSerArgSerAspGlyPheArgProAspTyrAlaGlyPheGluIleProHisLeu 186		
Db	549 AGACATCCGAACTGAGCTCTTGAACCTGACTATGCTGGATTGAGTTCAACCTTA 608		
Qy	187 PheValGlyLysTyrAlaLeuAspTyrAsnGluTyrPheArgAspLeuAsnHisIleCys 206		
Db	609 TTTGTGGTGGATGATGCTTAGATACATGATGATCTGATCTGATCATATGC 668		
Qy	207 -ValIleAsnGlu 210	BASE COUNT	193 a
Db	669 CGTCATCAATGAG 681	ORIGIN	114 c
Alignment Scores:		Length:	657
Bred. No.:	1.85e-76	Matches:	147
Score:	786.00	Percent Similarity:	30
Best Local Similarity:	83.49%	Conservative:	35
Query Match:	70.43%	Mismatches:	0
DB:	10	Indels:	0
RESULT 7	Gaps:	0	
CLHPT			
LOCUS	657 bp	mRNA linear	
DEFINITION	C. longicaudatus hprt mRNA for hypoxanthine (guanine) phosphoribosyltransferase.		
ACCESSION	X59652	CLHPT (1-657)	
US-09-902-705-2 (1-212) x CLHPT (1-657)			

(clonal) outgrowth infected with the virus MNTV."

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 62. .718
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BASE COUNT 380 a 230 c 272 g 399 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.27E-75 Length: 1281

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 Best Local Similarity: 68.87% Mismatches: 35
 Query Match: 70.07% Indels: 0
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US-09-902-705-2 (1-212) × EC004686 (1-1221)

Qy 1 MetA LleA ThrA ArgSer ProGlyValValIleLeuAspIrrpProGlyTyrAspLeuAsn 20
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 Db 62 ATGGCACCACCGCTTCAGCGCTGATTAAGCCATGTCACCGCTGATCACCTAGAT 121
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 21 LeuPheThrTyrProGlnHistYrrTyr-GlyAspLeuGluTrpValLeuLeuProHisGly 40
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 122 TGTGTTGATACOTAACTATTAGCCGAGATTGGAAAGTTTATCCCTATGAA 181
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 41 IleIleLeuAspArgTleGluAgleuAlaLysAspIleCysTyrSer 60
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 182 CIGATTAATGGAGCTGAGCTGAAAGCTGAGATCATGAGAGATGGAGGCCAT 241
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 Qy 61 AspIleMetValLeuCysValLeuLysGlyLysTyrIleAspCysSAlAspLeuValGlu 80
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 242 CACATGTCGCCCTCTGTGCTAAAGGGCTATAGCTTCTGCTGACTTGCGGAT 301
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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 302 TACATTAAGCAGTGTGATAGAATAGTGTGATGTCATCCATGACTGATGATTTATC 361
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 Db 101 ArgLeuLysSerTyrGalanAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120
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 362 AGCTGAGAGGCTACTCTATGTCATGCACTACGGGGCATAAAGTTATGGTGGAGAT 421
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Qy 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValValGlyGlyThrAla 140
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 Db 422 GATCTCTGAACTTAACTGAAAGATGCTTCATTTGAAAGATAATTGACACTCGT 481
 gene
 Qy 141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrIleAspAsnMetIleLysVal 160
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 Qy 161 AlaSerLeuLeuValIleLysArgThrSerArgSerAspGlyPheArgProAspTyrlAlaGly 180
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 542 GCAAGCTGCTGTGAAANGAACCTCGTGAAGTGTTGATAAGGCCAAAGCTTGTTGGA 601
 gene
 Qy 181 PheGluIleProHisLeuPheValAlaGlyTyrIleAsnGluTrpPheArg 200
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 gene
 Qy 201 AspLeuAsnHisIleCysValLeuAsnGluHisGly 212
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 LOCUS S43335 685 bp mRNA hypoxanthine phosphoribosyltransferase [cynomolgus monkeys, DEFINITION mRNA, 685 nt].
 ACCESSION S43335
 VERSION S43335.1 GI:254239
 KEYWORDS SOURCE Macaca fascicularis (crab-eating macaque)
 ORGANISM Macaca fascicularis
 Mammalia; Butheridae; Primates; Catarrhini; Cercopithecidae;
 Cercopithecinae; Macaca.
 REFERENCE 1 (bases 1 to 685)
 AUTHORS Harbach, P.R., Filipinas A.L., Wang, Y. and Aaron, C.S.
 TITLE DNA sequence analysis of spontaneous and
 N-ethyl-N-nitrosourea-induced hprt mutations arising in vivo in
 cynomolgus monkey T-lymphocytes
 JOURNAL Environ. Mol. Mutagen. 20 (2), 96-105 (1992)
 PUBLMED 150533
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI Gibbsq 111886] from the original Journal article.
 FEATURES Location/Qualifiers
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 1. .685
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Prod. No.:	1.13e-75				
Score:	779.00	Length:	685		
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Best Local Similarity:	68.40%	Conservative:	31		
Query Match:	69.80%	Mismatches:	36		
DDB:	9	Indels:	0		
Gaps:	0				
US-09-902-705-2 (1-212) x S433335 (1-685)					
Qy	1 MetAlaThrArgSerProGlyValValIleMetAspAspTyrPpProGlyTyraAspIleAsn 20				
Ddb	7 ATGGCGAICCCCAAGGCCCTGGCTCGTGTGATTAGGTGATGAAACGGTTAAGCTTGAT 66				
Qy	21 LeuPheThrTyrProGlnHisTyrTyrGlyAspIleGluGlyTyrValLeuIleProGly 40				
Ddb	67 TTATTCGATCATCTATCATATCTGAGGATTCTGGATTGCTGAGGTGTTATTCCTCATGCA 126				
Qy	41 IleLeuValAspArgIleGluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSer 60				
Ddb	127 CTAATATGGCAAGCTGAGCTGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCCAT 186				
Qy	61 AspIleMetValLeuCysValIleLysGlyGlyTyrLysPheCysAlaAspLeuValGlu 80				
Ddb	187 CACATTTGACCCCTGCTGCTGCTAGGGGGCTATAATTCTCTGCTGAGCTGGTGGAT 246				
Qy	81 HisIleLysSerIleSerArgLysSerAspArgPheValSerMetLysValAspPhenile 100				
Ddb	247 TAGATCAAGGACTCTGAAATAGTGTATGATGTCATCCTGATCTGAGATTTTCAT 306				
Qy	101 ArgIleIleSerTyrArgAspGlnSerMetGlyGluMetGlnIleGlyGlyGly 120				
Ddb	307 AGACTGAGACCTATGTAAATGACCTGAAAGGACATAAAAGTAATGGAGAGAT 366				
Qy	121 AspLeuSerThrIleAlaIleGlyLysAsnPheLeuIleValGluAspValValGlyThrGly 140				
Ddb	367 GATCTCTCAACTTAACTGGAAAGATGCTGATGTGTGAAAGATAATGACACCTGGC 426				
Qy	141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysAspAsnMetLeuIleVal 160				
Ddb	427 AAAACGATGAGCTGAGCTCTCTCTGTCAGCCACTATATCCAAAGATGTCAGGTC 486				
Qy	161 AlaSerIleLeuIleValGlyLysAsnGlySerArgSerAspGlyPheArgProAspTyrAlaGly 180				
Ddb	487 GCGAGCTTGCTGCTGAAAGACCTCACAAGTGTGATATACTGCAAGATCTGTCAGTATGATACTTCGG 546				
Qy	181 PheGluIleProHisIlePheValValGlyTyrTyrAlaLeuAspTyrAsnGluTyrPheArg 200				
Ddb	547 TTGAAATTCCAGAACAGTGTGCTCTAGATATGCCCTGACTATATGATACTTCGG 606				

Qy	201	AspLeuAsnHisIleCysValIleAsnGluHisGly	212
Db	607	: : : : : : : : : GATTGAACTAATGTTGTCATAGAACCTGA	642
RESULT 11			
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LOCUS	CL-longicaudatus	HPRT mRNA	linear
DEFINITION	CL-longicaudatus	for hypoxanthine guanine	ROD 21-MAY-1992
KEYWORDS	Phosphoribosyltransferase.		
ACCESSION	X17656	GI:49514	
VERSION	X17656.1		
SOURCE	Cricketulus longicaudatus (long-tailed hamster)		
ORGANISM	Cricketulus longicaudatus		
KEYWORDS	hypoxanthine-guanine phosphoribosyltransferase, point mutation.		
REFERENCE	Rossiter, F., Muzny, M., Caskey, T. and Fox, M.		
AUTHORS			
TITLE	A Chinese hamster HPRT point mutation reverts to the wild-type sequence		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1222)		
TITLE	Rossiter, F.		
JOURNAL	Direct Submission		
COMMENT	Submitted: 14-NOV-1989		
FEATURES	Rossiter B. J. F., Institute for Molecular Genetics, Baylor College of Medicine, 1, Baylor Plaza, Houston, Texas 77030, USA		
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	variation		

variation
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 1118 .1123 /Gene="HPRT"
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 Score: 779.00 Matches: 146
 Percent Similarity: 83.02% Conservative: 30
 Best Local Similarity: 68.87% Mismatches: 36
 Query Match: 69.80% Indels: 0
 DB: 10 Gaps: 0
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 Qy 21 LeuPheThrTyrProGlnHistYTYrGlyAspLeuGlyValLeuProHisGly 40
 Db 77 TTATTTGTTGATTCCTATCACTATGTCAGATTGAAAGGTTTTATCCCTATGAA 136
 Qy 41 IleLeuValAspArgLeuAlaLysAspPheAspIleGlyTyrSer 60
 Db 137 GRCATATTGACAGGGTGAAGACTGCGCGAGATGTCATGAAAGAGATGGAGGCCAT 196
 Qy 61 AspIleMetValLeuGlyValLeuLysAspCysAlaAspLeuValGlu 80
 Db 197 CRACATGTCGCCCTCTGTGTCGAAGGGGGCTATANATCTTGTGACTTGCTGGAT 256
 Qy 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspHelle 100
 Db 257 TACATTAAGCTGATGAAATACTGATCATGTCATCCCTGATCTGATTTATC 316
 Qy 101 ArgLeuLysSerTyrGlnAspGlnSerMetGlyGluMetGlnIleLeuGlyGlyGly 120
 Db 317 AGCTGAAGGCTTACCTTAATGTCAGTCAGCAAGGGCARAAAGTATTCGTTGGAT 376
 Qy 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValGlyThrGly 140
 Db 377 GATCTCTAACCTTAATGCAAGAAATGCTGATGTTGGCCATATTCACACTGTC 436
 Qy 141 ArgThrMetLysAlaLeuSerAsnIleLeuLysTyrLysProAsnMetIleuVal 160
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 Qy 161 AlaSerLeuLeuValLysArgThrSerArgSerAspGlyPheArgProAspTyrAlaGly 180
 Db 497 GCTAGCTTGTCTGTTGAAAGGACCTGAAAGCTCCGAGTGTGGATATGCCCGAACCTGTTGCA 556

Qy 181 PheGluIleProHisLeuPheValGlyValAlaLeuAspTyrAsnGlyLysTyrPheArg 200
 Db 557 TTGGAATTCGACAGCAAGATTTCTGCTGATATCCCTGACTTAAAGCTACTTCG 616
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 LOCUS BC000578 DEFINITION Homo sapiens, hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome), clone MGCI:7122 IMAGE:3161726, mRNA, complete cds.
 ACCESSION BC000578
 VERSION BC000578.1 GI:112653662
 KEYWORDS MGCI
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1316)
 REFERENCE 1 (bases 1 to 1316)
 AUTHORS Strasberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC). Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 COMMENT Contact: MGC help desk
 Tissue: cgabbs-r@mail.nih.gov
 CDNA Library Preparation: Rubin Laboratory
 DNA Procurement: ATCC
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc_mgc@nghri.nih.gov
 Shevchenko, Y., Wetherby, D., Beckstrom-Sternberg, S.M., Benamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlin, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastilo, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tiongson, E.B., Touchman, J.W., Tsugeon, J.C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINN at: http://image.llnl.gov Series: IRBL Plate: 5 Row: m Column: 19
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504482.
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 1. .1316
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 /mol_type="mRNA"
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Db 271 CACATGTCGCCCTCTGCTAAAGGGCTATAATTCCTGCTACCTGCGGGAT 330
Qy 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspHelle 100
Db 331 TACATTAAGCAGTGTAGATAAGTATGATCATCCATCCCCTCACTAGTTATTC 390
Qy 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120
Db 391 AGACTGAAAGGCTACTGTAGCTAATGTCAGTCACAGGGCACAAGGTATGCTGGGAT 450
Qy 121 AspLeuSerThrIleAlaIgIyLysAsnPheLeuIleValGluAspValGlyThrGly 140
Db 451 GATCTCTCAACTTAACTGAAAGAATGCTGATTTGATGAGCATATAAACCTGGT 510
Qy 141 ArgThrMetLysAlaLeuLeuSerAsnIleGlyItyrsProAsnMetIleLysVal 160
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Qy 161 AlaSerIleLeuValLysArgThrSerAspGlyPheAspProAspPheAlaGly 180
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Qy 181 PheGluIleProHisLeuPheValIleGlyItyrAlaLeuAspTyrAsnGlyIlePheArg 200
Db 631 TTGGAAATTCGAGAGTTGCTGAACTGCTGAACTGTTGCAATAGCTAAATGCTCAGG 690
Qy 201 AspLeuAsnHisIleCysValLeuAsnGluHisGly 212
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Search completed: October 4, 2003, 13:38:52
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